

SQ	Sequence 1638 AA;	CC	from WIPO at ftp.wipo.int/pub/published_pct_sequences
XX	Query Match 10.2%; Score 138; DB 4; Length 1638;	SQ	Sequence 758 AA;
XX	Best Local Similarity 21.2%; Pred. No. 0.00033; Mismatches 100; Indels 72; Gaps 13;	XX	Query Match 9.2%; Score 125; DB 4; Length 758;
XX	Matches 58; Conservative 43; Mismatches 100; Indels 72; Gaps 13;	XX	Best Local Similarity 25.6%; Pred. No. 0.0235; Mismatches 93; Indels 62; Gaps 13;
Qy	3 KILVGFAEVVVSADSVHRLCLSACLNAFDTPGFRCESMVWYYPDAECILNTEDRDRDLP 62	Qy	1 CLSACLNAAFDPGFCESMVWYYPDAECIL-NEDRDRDLPFDENEDTVIYLDNCA 78
Db	211 KLPISDKITAAANR-SDCEDKLN--EFSIVCRSANFSNDFRSCLRSRTRTHPEM 266	Db	160 CLEAC---QANESCSA VANY-ETGLCWMFRSTADQLP-GSLRSQYPVFTVAKSCF 211
Qy	63 VDEPHEDTVIYLDNCAAGCECHWHFDNFNKTSGLNDQFAIAACQCYAPVTOVAVEGRL 122	Qy	79 G---CECHWHFDNFNKTSGLNDQFAIAACQCYAPVTOVAVEGRLQSBDLHSFGEEL 135
Db	257 EDPNSD--YIENITCLNAE-----RRCDG-LAVIVKEENKRL 300	Db	212 GVRPCKSAWCIDR-----VQYTRPERAKASQVATR 243
Qy	123 SD--ELDHSFEGELBLSECEELCTQRLSVAFTANDFNCKSFMSYNSLTSCLSDRS-RPLGR 179	Qy	136 SBECEELCTQRLSVAFTANDFNCKSFMSYNSLTSCLSD-ERSRPLGRNLAVPGWNTYFESR 194
Db	301 GGPFEVD-I FNNTL EECQTM-----LRAEKYFCRSVEFDQSKOCLSEEDSISQDD 354	Db	244 RDCIERG---LGETEFTCRSANYTAHSGLCELSDDMRTISBANIAA YGDYLENN 298
Qy	180 ANIAEVECWYTFE-----SRGPFSFIRVQMLVGPASP 213	Qy	195 GV--PS---FTRVQMLVGPASP TMENYNPVNTCLDQCTSPPPETGQNFVCKSWMYK 248
Db	355 ISISSSPTHFVYDLCUCLNQRANDYPDNSVTSHLFSSGRRPDTAFORYRNSRLGGFPHSE 414	Db	299 CAAEPSKLCF KVRAGRLKTVDS-VHQNQVTLDBCRDILTAP-----FRCHS---VYD 349
Qy	214 VMEVNVPSTWMCLDQCTSPPPETQNFVCKSWMY 246	Qy	249 NE 250
Db	415 INGR--SUSECDECIRQ-----TSFQCRSAVY 440	Db	350 NR 351
RESULT 2		RESULT 3	
XX	ABB58337	XX	ABB50426
XX	ABB58337 standard; protein; 758 AA.	XX	ABB50426 standard; protein; 744 AA.
AC	ABB58337;	AC	ABB50426;
XX	DT 26-MAR-2002 (first entry)	XX	DT 26-MAR-2002 (first entry)
XX	DE Drosophila melanogaster polypeptide SEQ ID NO 1803.	XX	DB Drosophila melanogaster polypeptide SEQ ID NO 2070.
KW	kw: developmental biology; cell signalling; insecticide; pharmaceutical.	KW	kw: developmental biology; cell signalling; insecticide; pharmaceutical.
OS	os: Drosophila melanogaster.	OS	os: Drosophila melanogaster.
XX	PN WO200171042-A2.	XX	PN WO200171042-A2.
XX	PD 27-SEP-2001.	PD 27-SEP-2001.	
XX	PR 23-MAR-2001; 2001WO-US009231.	PR 23-MAR-2001; 2001WO-US009231.	
XX	PR 11-JUL-2000; 2000US-00614150.	PR 23-MAR-2000; 2000US-0191637P.	
PA	(PEKE) PE CORP NY.	PR 11-JUL-2000; 2000US-00614150.	
XX	PR 23-MAR-2000; 2000US-0191637P.	XX	PR 23-MAR-2001; 2001WO-US009231.
PA	PR 11-JUL-2000; 2000US-00614150.	XX	PR 11-JUL-2000; 2000US-00614150.
PI	Venter JC, Adams M, Li PWD, Myers EW;	XX	PR 11-JUL-2000; 2000US-00614150.
XX	DR WPI; 2001-656860/75.	XX	PR 11-JUL-2000; 2000US-00614150.
DR	DR N-PSDB; ABL02440.	XX	PR 11-JUL-2000; 2000US-00614150.
XX	PT Disclosure: SEQ ID NO 1803; 21pp + Sequence Listing; English.	XX	PR 11-JUL-2000; 2000US-00614150.
PT	PT New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.	XX	PR 11-JUL-2000; 2000US-00614150.
PT	PT The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (AB57737-CC ABL7207). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly	XX	PR 11-JUL-2000; 2000US-00614150.
CC	CC The invention relates to an isolated nucleic acid detection reagent useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (AB57737-CC ABL7207). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly	XX	PR 11-JUL-2000; 2000US-00614150.
CC	CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions.	XX	PR 11-JUL-2000; 2000US-00614150.
CC	CC Disclosure: SEQ ID NO 2070; 21pp + Sequence Listing; English.	XX	PR 11-JUL-2000; 2000US-00614150.
CC	CC New isolated nucleic acid detection reagent for detecting 1000 or more genes from Drosophila and for elucidating cell signaling and cell-cell interactions.	XX	PR 11-JUL-2000; 2000US-00614150.
CC	CC The invention relates to an isolated nucleic acid detection reagent capable of detecting 1000 or more genes from Drosophila. The invention is useful in developmental biology and in elucidating cell signalling and cell-cell interactions in higher eukaryotes for the development of insecticides, therapeutics and pharmaceutical drugs. The invention discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA sequences (ABL01840-ABL16175) and the encoded proteins (AB57737-CC ABL7207). The sequence data for this patent did not form part of the printed specification, but was obtained in electronic format directly	XX	PR 11-JUL-2000; 2000US-00614150.

CC ABB72072]. The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences
 XX sequence 744 AA;

Query Match 8.9%; Score 121; DB 4; Length 744;
 Best Local Similarity 23.4%; Pred. No. 0.0061; Mismatches 102; Indels 78; Gaps 14;
 Matches 64; Conservative 29; MisMatch 102; Indels 78; Gaps 14;
 Qy 5 LVGFAREVVA-----DS-----VHRCISACLNADFTRGPFECBSVMMYPVDAEC 43
 Db 117 LVGF-----EIVIGYVFSAPEKLMDSQPGTLMITDCLDTCRK-----NKTQSVNY-----ETGLC 167
 Qy 49 ILNEDRLRPP-----LVDEREDTIVYLDNNCAG-----CECHWHDPKTSGLNIDQFATAA 104
 Db 168 VLFSAHADOLPGLALKSQQFVFTIQAQKSLAVKPCSRRAWYDR----- 211
 Qy* 105 QCYAPYVTVQVAVEGRQLSDELDHSFEGELBSCEELCTORLSVTANDNCNSKMSNLT 164
 212 -----VQVYKLTKEVKRVSASRRECELC-----LGENDFTCRSANYDRS 254
 Qy 165 RSCVLSDERSRPLGRNLAEV-----PGTYFESRGVP-----SFRVQPMIUVGAFSPVMN 217
 Db 255 GACELSELDRLLTAGSQAQVNDGSDYLENHCVDENPKLCEFPKLUPGRILKTVDS-VYOE 313
 Qy 218 VPSVVMCLDQTSPPETGONFVCKSVMYNE 250
 Db 314 VSIDCREBLNSP-----YRCHS-----YDYN 338

RESULT 4

ABB70535 standard; protein; 692 AA.
 XX AC ABB70535;
 XX DT 26-MAR-2002 (first entry)
 XX DE Drosophila melanogaster polypeptide SEQ ID NO 38397.
 XX KW Drosophila; developmental biology; cell signalling; insecticide;
 XX KW pharmaceutical.
 XX OS Drosophila melanogaster.
 XX PN WO200117042-A2.
 XX PD 27-SEP-2001.
 XX- PR 23-MAR-2001; 2001WO-US009231.
 XX PR 23-MAR-2000; 2000US-0191637P.
 PR 11-JUL-2000; 2000US-00614150.
 XX PA (PEKE) PE CORP NY.
 XX PI Venter JC, Adams M, Li PWD, Myers EW;
 XX DR WPI; 2001-65660/75.
 DR N-PSDB; ABL14638.
 XX PT New isolated nucleic acid detection reagent for detecting 1000 or more
 PT genes from Drosophila and for elucidating cell signalling and cell-cell
 PT interactions.
 XX PS Disclosure; SEQ ID NO 30397; 21pp + Sequence Listing; English.

CC The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention

CC discloses genomic DNA sequences (ABL16176-ABL30511), expressed DNA
 CC sequences (ABL0180-ABL1617) and the encoded proteins (AB57737-
 CC AB572072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at ftp.wipo.int/pub/published_pct_sequences

SQ Sequence 692 AA;

Query Match 8.9%; Score 120.5; DB 4; Length 692;
 Best Local Similarity 19.9%; Pred. No. 0.0062; Mismatches 92; Indels 87; Gaps 9;
 Matches 53; Conservative 35; MisMatch 92; Indels 87; Gaps 9;
 Qy 3 KILVGFAREVVSADSVHRCISACLNADFTRGPFECBSVMMYPVDAECILNTEDRUDRDPDF 62
 Db 118 KVIRGLDNALIYVJSTKACLSACN-----ERRFVCRSEVDYNNKCVLSDSDRASSGQEV 174
 Qy 63 VDEHEBDTVYLDNNC-----AGCECHWHDPKTSGLNIDQFATAAQCYAPYVTVQAVAE 211
 Db 175 OLIVDQGTDIFENICLKPKAQACKNSRFSQNSQRMGVSEEK-----VAQYVGL- 221
 Qy 119 GRQLSDELHSFEGELBSCEELCTORLSVTANDNCNSKMSNLTR----- 165
 Db 222 -----HYVTDKELQVTSSEACRLACEIESFLCRSFLYQGQPOQSQYNCRLYHLDH 272
 Qy 166 -----SCVLSDERSRPLGRNLAEV-----PGTYFESRGVP-----GVSFTRVHQ 204
 Db 273 KTLPGPSVTLNHRPLDNGEPIGQ-----YFENQCBKAAGLGLAGSPPGT--- 318
 Qy 205 MLVGFASFTMENYPSVTKLQDCTSP 231
 Db 319 -----LDKIDTLPSLDTIEDP 335

RESULT 5

AAG67230 standard; protein; 790 AA.

ID AAG67230;

XX AC AAG67230;

XX DT 13-NOV-2001 (first entry)

XX DE Amino acid sequence of pig plasminogen.

XX Angiostatin; plasminogen; sulphydryl donor; angiogenesis; tumour;
 KW angiogenic disease; neoplastic disease; connective tissue disorder;
 KW rheumatoid arthritis; atherosclerosis; ocular angiogenic disease;
 KW diabetic retinopathy; corneal graft rejection; cardiovascular disease;
 KW cerebral vascular disease; diabetes; immune disorder;
 KW chronic inflammation; autoimmunity.
 XX OS Sus scrofa.
 XX PN WO200159321-A2.
 XX PR 16-AUG-2001.
 XX PP 08-FEB-2001; 2001WO-US004021.
 XX PR 08-FEB-2000; 2000US-00500397.
 XX PA (NOUN) UNIV NORTHWESTERN.
 XX PI Soff G, Gately ST, Twardowski P;
 XX PR WPI; 2001-550019/51.
 XX DR

PT Producing angiostatin for treating angiogenic disease involves
 PT contracting plasminogen with plasminogen activator and sulphydryl
 PT donor.
 XX PS Disclosure; Page 77-80; 101pp; English.

CC The specification describes a method for generating angiostatin in vitro.
 CC The method comprises contacting plasminogen with a sulfonyl donor, or
 CC culturing cells capable of producing plasminogen activator in conditioned
 CC culture medium (CCM) and contacting the CCM with plasminogen. Angiostatin
 CC produced by method of the invention is useful for treating animals with
 CC angiogenesis diseases. It is useful for treating an angiogenic disease
 CC such as neoplastic diseases (e.g. tumours and tumour metastasis), benign
 CC tumours (e.g. hemangiomas, acoustic neuroomas, etc), connective tissue
 CC disorders (e.g. rheumatoid arthritis and atherosclerosis), ocular
 CC angiogenic diseases (e.g. diabetic retinopathy, corneal graft rejection,
 CC (etc), cardiovascular diseases, cerebral vascular diseases, diabetes-
 CC associated diseases and immune disorders (e.g. chronic inflammation and
 XX autoimmunity). The present sequence represents a plasminogen
 SQ Sequence 790 AA;

Query Match 8.6%; Score 116; DB 4; Length 790;

Best Local Similarity 19.5%; Pred. No. 0.021; Mismatches 100; Indels 84; Gaps 12;

Matches 55; Conservative 43; Mismatches 100; Indels 84; Gaps 12;

QY 5 LIVGFARENSADSVAHRCISACAINAFDFTFGFETESVMYVPVDAECLINTEDRLLRDPFLVD 64

Db 14 LFSLSRKQVAARVEECAAKC-EAET-NFICRAFQVHSKQDQCVMWAENGKTSPIA 67

QY 65 EHEDTV-----TVDNNCAGCCECHWHFDNFKRSQGILNDQQAIAQCTIACQYAPTYQVAVEG 119

Db 68 RMRDVVLFEKRKYLSECKTGNGKMYRGTTSKTSQGVICQKNSVSPHPIKYSPEKPLAG 127

QY 120 RQ-----LSDEDHSTEGLESECEBLCTQ-----RIVSTANDFNC 155

Db 128 LSEENYCRNPNDBKGPWCYTDPETRFDYCDIPCEDECBCMHSGEHYEGKISKTMGIEC 187

QY 156 Ks-----PMYSNITRS-CVLSRSRSLGRANLAEVPGWTFYFESRGVPSP 199

Db 188 QWGSQSPHAGYPLSKPKNLQKMYCRNPGEPRP-----W-----CF 227

QY 200 TRVQMLLVGFASFVMEVPSVYMCUDQCTSPPPETCQNFYC 241

Db 228 TTDPN-----KRMFCDIP-----RCTIPPTSGPTYQC 256

RESULT 6

ABB58185

ID ABB58185 standard; protein; 833 AA.

XX

AC ABB58185;

XX

DT 26-MAR-2002 (first entry)

XX

DE Drosophila melanogaster polypeptide SEQ ID NO 1347.

XX

KW Drosophila; developmental biology; cell signalling; insecticide;

XX

KW pharmaceutical.

XX

OS Drosophila melanogaster.

XX

DN W0200171042-A2.

XX

PD 27-SEP-2001.

XX

PP 23-MAR-2001; 2001WO-US0009231.

XX

PR 23-MAR-2000; 2000US-019137P.

XX

PR 11-JUL-2000; 2000US-00614150.

XX

PA (PEKE) PE CORP NY.

XX

PT Venter JC, Adams M, Li PWD, Myers EW;

XX

PT WPI; 2001-656860/75.

XX

DR N-PSDB; ABL02288.

XX

PT New isolated nucleic acid detection reagent for detecting 1000 or more

CC genes from Drosophila and for elucidating cell signaling and cell-cell
 CC interactions.

CC Disclosure: SEQ ID NO 1347; 21pp + Sequence Listing; English.

CC

XX The invention relates to an isolated nucleic acid detection reagent
 CC capable of detecting 1000 or more genes from Drosophila. The invention is
 CC useful in developmental biology and in elucidating cell signalling and
 CC cell-cell interactions in higher eukaryotes for the development of
 CC insecticides, therapeutics and pharmaceutical drugs. The invention
 CC discloses genomic DNA sequences (ABL1840-ABL16176-ABL130511), expressed DNA
 CC sequences (ABL1840-ABL16176-ABL130511), and the encoded Proteins (ABL5777-
 CC ABB72072). The sequence data for this patent did not form part of the
 CC printed specification, but was obtained in electronic format directly
 CC from WIPO at http://wipo.int/pub/published_pct_sequences

XX

SQ Sequence 833 AA;

Query Match 8.3%; Score 113; DB 4; Length 833;

Best Local Similarity 23.2%; Pred. No. 0.056; Mismatches 98; Indels 76; Gaps 15;

Matches 63; Conservative 34; Mismatches 98; Indels 76; Gaps 15;

QY 3 KILVGFARENSADS-----VHRQISACINAFTDFGFGECSVMYVPVDAECL- 50

Db 122 EILIGY--VLSAASKMLPMLPGLMLTLCLEAQS----NESCSAVY--EYGLCVIF 171

QY 51 -NTEDRLRDPFLVDEHEDHEDVYIILDNNCAG--CCECHWHFDNFKRSQGILNDQQAIAQAC 106

Db 172 KITADKLK-GSLRSQSPVPTIYQKSCGVRPGCSKAWKIDR----- 212

QY 107 YAPVYIQQVAVEGRLSDLDHSTEGLESECEBLCTQSLSVTANDEKNSKFSMYSNLTRS 166

Db 213 -----VQYRLPPEAVKSSQTVLSRDRCLC-----LGBTEFTCRSANYVRHSGI 257

QY 167 CVLSD-ERRPLGRPLGRANLAEVPGWTFYFESGV-PS-----FTRPQMLLVGFASFVMEWP 219

Db 258 CELSDMDRILTSAGGSVEPYDGBYLENNCAEPBSKLCEFKRISGKILKTVDS-VYQDN 316

QY 220 SVTMCLDQCTISPPPBETGQIVFVCKSVMYVYNE 250

Db 317 TIDEGRDCLNSP-----YRCHS--YDYN 339

RESULT 7

AY50872

ID AY50872 standard; protein; 812 AA.

XX

AC AY50872;

XX

DE 24-FEB-2000 (first entry)

XX

DE Bovine plasminogen protein fragment.

XX

KW Plasminogen; bovine; thrombolytic agent; streptokinase; antigenic;
 KW blood clot; heart attack; treatment.

XX

OS Bos tauriB.

XX

PN WO957251-A2.

XX

PD 11-NOV-1999.

XX

PR 06-MAY-1999; 99WO-US010086.

XX

PR 06-MAY-1998; 98US-0084392P.

XX

PA (OKLA-) OKLAHOMA MEDICAL RBS FOUND.

XX

PI Zhang XC, Lin X, Tang JUN;

XX

DR WPI; 2000-052966/04.

XX

PT New thrombolytic agents derived from modified humanized streptokinase,

XX
DE Plasminogen protein for production of recombinant plasminogen.
XX
KW Plasminogen; alpha-1-antitrypsin; AAT; argaserpins; recombinant;
KW stabilising protein.
XX
OS Homo sapiens.
XX
PH Location/Qualifiers
PT Misc-difference 60 /note="encoded by ACC"
PT Misc-difference 191 /note="encoded by GAA"
PT Misc-difference 223 /note="encoded by AAA"
PT Misc-difference 280 /note="encoded by GCT"
PT Misc-difference 291 /note="encoded by CTG"
PT Misc-difference 395 /note="encoded by GSA"
PT Misc-difference 503 /note="encoded by CAG"
PT Misc-difference 607 /note="encoded by TCT"
PT Misc-difference 615 /note="encoded by CAG"
PT Misc-difference 658 /note="encoded by TTG"
PT Misc-difference 709 /note="encoded by GCT"
PT US5648254-A.
XX
PN 15-JUL-1997.
XX
PP 14-JUL-1994; 94US-0275076.
XX
PR 04-JAN-1988; 88US-0144357.
PR 04-DEC-1989; 89US-0145302.
PR 28-OCT-1991; 91US-0185865.
XX
PA (ZYMO) ZYMOGENETICS INC.
PI Kumar AA, Mulvihill ER;
XX
DR WPI; 1997-372063/34.
DR N-REDB; AAT89886.
XX
PT Production of recombinant plasminogen - by co-expression with plasminogen
PT -processing or -stabilising protein.
XX
PS Example 2; FIG 6A-D; 32pp; English.
XX
CC This is the protein plasminogen. The encoding cDNA is used in a new
process for the production of plasminogen where a first DNA sequence
encoding plasminogen and at least one additional DNA sequence encoding a
protein that processes or stabilizes the plasminogen is introduced into a
eukaryotic host cell. The protein is selected from alpha-1-antitrypsin
(AAT) and its variants and Argaserpins. Both the DNA sequences are
operably linked to transcriptional promoter and terminator sequences. The
host cell is cultured under conditions that allow the DNA sequences to be
expressed and the recombinant plasminogen is isolated from the host cell.
CC Co-expression of plasminogen and the protein gives increased yields of
CC undegraded plasminogen
XX
SQ sequence 810 AA;

Query Match 7.5%; Score 102; DB 2; Length 810;
Best Local Similarity 17.7%; Pred. No. 0.57;
Matches 52; Conservative 45; Mismatches 89; Indels 108; Gaps 12;

Db 3.3 LFSVTKKQIGAGSIEBCKACEDEEE--FYCRAFOYHSREQQVIMABRNKSSIIIRW 89
Qy 60 DLFVDEBEHTVIVLDNNCAGCCECHWFDNFKTSILNDQFATAAQCVAPVYQVAVG 119
Db 90 DVLFEKK--VLISECKINGKQYRTGNTSKTKGITCKWSS- 113
Qy 120 RQLSDELDHSPEGIE-----LSECEFLCTO----- 144
Db 134 RPRSPATRPSSEGLENCRNPNDPQGFWCYTDPKRYDQILECEBECMCGGY 193
Qy 145 --RUSVTANDPNCKS-----FMTSNTLRSCLVSDERSRSLGRANLAEVIG 187
Db 194 DGKLSKTMGSGLECAWDSQSPHANGYIPSCFPNKNLKGKNCRNP-----ELRP 243
Qy 188 WTYFBRSRGVPSFRVQPMILVGEASFVMEVNPSVTCMLQCTSPPEQNFVC 241
Db 244 W-----CFTIDPN-----KAWECDIP-----RCTRPPPSGPTYOC 275

RESULT 12
AAR60519
ID AAR60519 standard; protein; 790 AA.
XX
AC AAR60519;
XX
DT 25-MAR-2003 (revised)
DT 22-MAR-1995 (first entry)
XX
DB Human 'G3u' Plasminogen.
XX
KW Serine protease; Factor-Xa; recognition site; plasminogen; kringle;
KW fusion protein cleavage; protein folding; primer;
KW polymerase chain reaction; amplification.
XX
OS Homo sapiens.
XX
PN W09418227-A2.
XX
PD 18-AUG-1994.
XX
PP 04-FEB-1994; 94WO-DK000054.
XX
PR 04-FEB-1993; 93DK-00000130.
PR 05-FEB-1993; 93DK-00000139.
PR 03-DEC-1993; 93WO-GB002492.
XX
PA (DENZ-) DENZYME A8S.
XX
PI Thøgersen HC, Holtet TL, Bæzerodt M;
XX
DR WPI; 1994-279681/34.
XX
PT Refolding of polypeptide molecules - using a cyclic process involving
PT denaturing and renaturing conditions to produce a correctly folded prod.
XX
PS Disclosure; Page 148-50; 202pp; English.
XX
CC cDNA encoding kringle domains 1 and 4 of human plasminogen (full sequence
given in AAR60519) was PCR amplified using primers given in AAR7126-71.
CC Amplified cDNA was linked to a sequence encoding the Factor-Xa cleavage
site (given in AAR60503), subcloned in vector pCMVICH so that it was
linked to a hexahistidine-encoding sequence and expressed in E. coli
QY13. The fusion protein was purified on an Ni2+-activated NTA-agarose
column. A cyclic procedure was used to obtain correctly folded
CC recombinant protein. (Updated on 25-MAR-2003 to correct PN field.)
XX
SQ sequence 790 AA;

Query Match 7.5%; Score 101.5; DB 2; Length 790;
Best Local Similarity 18.0%; Pred. No. 0.62;
Matches 53; Conservative 42; Mismatches 90; Indels 109; Gaps 13;

Query Match 7.5%; Score 101; DB 7; Length 480;
 Best Local Similarity 18.0%; Pred. No. 0..36; Mismatches 90; Indels 110; Gaps 13;
 Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

QY 5 LVGFAREVVSADSVRCLSLACTNAFDITFGFBCESVMYVFDAAECLNTEDR---LDRPD 60
 14 LFSVTKKQLGAGSIECAKEEDEB--FTCRAFOYHSKEQQCVIMAENRKSSIIIRMD 70
 61 LVFDDEHEDTVTVDNNCAGCCHWHDNFNKQSKGILNDQFATAOCYAPYVTOVYAVEGR 120
 71 VVLFERK---VYSECKITGNGKNGYRGTMSKTKNGITCOKWSST---SPH-----R 114
 Db 121 QLSDELDHSFEGLE-----LSCCELTQ----- 144
 Db 115 PRFSRPATHPSGLEENYCRNPNDPQGPWCYTDPKRYDYCCDILBCEBECMHCSGENYD 174
 QY 145 -RLSVTANDFNCKS-----FMISNLTRS-CVLSDESRPLGRANLAEVPG 187
 Db 175 GRSKISITMGLCQAWQSQSOPSPHAGYIIPSKFERNLKNLKGNYCRNPNDPDRLRP----- 223
 QY 188 WTYFESRGVPSTTRVPQMLLVGFFASFVNMENVSVMVTMCLDQCTSPPEGTQNFVC 241
 Db 224 W-----CFTDPN-----KRWELCDIP-----RCTTPPPSSGPTYQC 255
 RESULT 13
 ID ABU64288 standard; protein: 480 AA.
 XX ABU64288;
 XX ABU64288 standard; protein: 480 AA.
 AC AC
 DT 11-MAR-2004 (first entry)
 ID ID
 DE Human angiostatin protein.
 XX
 KW Vector; rAAV; recombinant adeno-associated viral vector;
 KW anti-angiogenesis; pRNP; angiogenesis; eye disorder; blindness;
 KW retinal degeneration; macular degeneration; neovascularisation;
 KW ophthalmological.
 OS homo sapiens.
 XX WO2003080648-A2.
 XX PD 02-OCT-2003.
 XX PF 20-MAR-2003; 2003WO-US008667.
 XX PR 20-MAR-2002; 2002US-0366114P.
 XX PA (UYFL) UNIV FLORIDA RES FOUND INC.
 PA (UYJO) UNIV JOHNS HOPKINS.
 XX PI Hauswirth WW, Campochiaro PA, Berns KI;
 XX DR WPI; 2003-779243/73.
 XX PT Novel adeno-associated viral vector comprising polynucleotide encoding
 PT pigment epithelium-derived factor, useful for treating choroidal
 PT neovascularization, blindness, loss of vision.
 XX PS Claim 14; Page 37; OPP; English.
 CC The present invention relates to an adeno-associated viral (AAV) vector
 CC comprising a polynucleotide that comprises a nucleic acid segment that
 CC encodes a choroidal or ocular neovascularisation inhibitory polypeptide
 CC operably linked to a promoter that expresses the segment to produce the
 CC polypeptide in a selected mammalian host cell. Such a vector is useful
 CC for providing a choroidal or ocular neovascularisation inhibitor
 CC polypeptide to a mammal, for use in the therapy of ocular
 CC neovascularisation, choroidal neovascularisation, retinal
 CC dysfunction, age-related macular degeneration, visual impairment,
 CC ocular dysfunction, loss of vision, retinopathy, or blindness in a human.
 CC The present sequence is a protein shown in the exemplification of the
 CC invention
 XX Sequence 480 AA;

RESULT 14
 ID ABB75942 standard; protein: 563 AA.
 AC ABB75942;
 XX ABB75942;
 DT 01-JUL-2002 (first entry)
 DE Endothelial cell growth inhibitor, angiogenesis.
 XX KW Plasminogen; angiogenesis; inhibitor; tumour; antitumour;
 KW cytostatic; antipsoriatic; dermatological; ophthalmological;
 KW antidiabetic; antiarthritic; vulnerary; antiulcer; antiatherosclerotic;
 KW contraceptive; gene therapy; human.
 XX OS Homo sapiens.
 XX SYNTETIC.
 PH Key Location/Qualifiers
 PT Peptide 1..32
 PT /label= Signal_peptide
 PT Peptide 33..96
 PT /label= Pre-activation_peptide
 PT Domain 97..560
 PT /label= Kringles_1-6
 XX WO200220813-A2.
 XX PD 14-MAR-2002.
 XX PR 31-AUG-2001; 2001WO-EP010090.
 XX PR 05-SEP-2000; 2000US-0230893P.
 XX PA (KARO-) KAROLINSKA INNOVATIONS AB.
 XX PI Cao Y;
 XX DR WPI; 2002-362251/39.
 XX PT Novel recombinant protein termed angiogenesis useful for treating tumor,
 PT ulcer, comprises amino acid sequence corresponding to Kringle 1-5,
 PT secretory signal peptide and pre-activation peptide of mammalian
 PT plasminogen.
 XX PS Claim 6; FIG 6; 63PP; English.

CC The present sequence is the protein sequence of a novel recombinant
 CC endothelial cell growth inhibitor, termed angiogenesis, which comprises
 CC the signal peptide and pre-activation peptide of plasminogen (see
 CC ABB75939) in association with Kringle 1-5. Angiogenesis may also
 CC include a C-terminal tumour-targetting peptide (see ABB7543-44).
 CC Angiogenesis, nucleic acids encoding it, vectors and host cells are used
 CC in the preparation of a medicament for treating a tumour by preventing
 CC angiogenesis (claimed). In claimed methods, the peripheral and tumour-
 CC infiltrating lymphocytes, hepatocytes, epidermal cells, myocytes or other
 CC somatic cells of a patient in need of anti-angiogenic therapy are
 CC transfected with a viral (especially retroviral) vector comprising an
 CC angiogenesis nucleic acid, and the transfected cells are then expanded
 CC and implanted into the patient. Angiogenesis is useful for inhibiting
 CC cancer metastasis, and for treating angiogenesis associated conditions
 CC such as tumour growth, e.g., cancer, diabetes, etc. It is also useful for
 CC treating haemangioma, solid tumours, leukaemia, psoriasis, scleroderma,
 CC arteriovenous malformations, rubosis, neovascular glaucoma, diabetic
 CC retinopathy, arthritis, diabetic neovascular macular degeneration, wound healing, peptic ulcer, intestinal adhesions,
 CC arteriosclerosis, fractures, keloids, vasculogenesis, haemopoiesis or
 CC scratch fever. The protein can also be used as a birth control agent
 CC by preventing the vascularisation required for embryo implantation. The
 CC half maximal concentration (BC50) of angiogenesis for inhibiting
 CC endothelial cell proliferation is about 50 pM, compared with 100 nM for
 CC angiostatin
 XX sequence 563 AA;

Query Match 7.5%; Score 101; DB 5; Length 563;
 Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;
 QY 5 LVGFARREVVSADSVRCLSLACLNADTFEGECESVMYYPVDAECLNTEDR----LDRP 59
 Db 33 LFSVTRKKQLGAGSIEBAAKCEEDEE--FICRAFOYHSKQOCVIMAENRKSSIIIR 89
 SQ

QY 6 DLFVDEHEDTVYILDNNCAGCCEHHWDFDNFKTSGLNDQOFAIAQCYAPYVTOVAVEG 119
 Db 90 DVLFEKK--VYLSCECKTGNGKVRGTMNSKTKNGITCKWST---SPH----- 133
 QY 120 RQLSDELDISFEGLE-----LSECELCTQ----- 144
 Db 134 RPRSPATHSEGLBENYCRNPNDPQGPWCYTDPKRYDYCILEBECMHCSGENY 193
 QY 145 --RLSVTANDPNCKS-----FMYSNLTTS-CVLSDRSPPLGRANLAEP 186
 Db 194 DGKSKRTMSGLEQWDSOPHAGHYIPSKRPPKNNLKNYCRNPDRRLP----- 243
 QY 187 GWTYFESRGVPSFRVPQMLVGFASPVFMENVPVSTMCIDQCTSPPPETQONFVC 241
 Db* 244 -W-----CFTDPN-----KRWELCDIP-----RCTTPPSSGPTYQ 275
 SQ

Query Match 7.5%; Score 101; DB 2; Length 566;
 Best Local Similarity 18.0%; Pred. No. 0.45; Mismatches 90; Indels 110; Gaps 13;
 Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

QY 5 LVGFARREVVSADSVRCLSLACLNADTFEGECESVMYYPVDAECLNTEDR----LDRP 59
 Db 33 LFSVTRKKQLGAGSIEBAAKCEEDEE--FICRAFOYHSKQOCVIMAENRKSSIIIR 89
 QY 6 DLFVDEHEDTVYILDNNCAGCCEHHWDFDNFKTSGLNDQOFAIAQCYAPYVTOVAVEG 119
 Db 90 DVLFEKK--VYLSCECKTGNGKVRGTMNSKTKNGITCKWST---SPH----- 133
 QY 120 RQLSDELDISFEGLE-----LSECELCTQ----- 144
 Db 134 RPRSPATHSEGLBENYCRNPNDPQGPWCYTDPKRYDYCILEBECMHCSGENY 193
 QY 145 --RLSVTANDPNCKS-----FMYSNLTTS-CVLSDRSPPLGRANLAEP 186
 Db 194 DGKSKRTMSGLEQWDSOPHAGHYIPSKRPPKNNLKNYCRNPDRRLP----- 243
 QY 187 GWTYFESRGVPSFRVPQMLVGFASPVFMENVPVSTMCIDQCTSPPPETQONFVC 241
 Db 244 -W-----CFTDPN-----KRWELCDIP-----RCTTPPSSGPTYQ 275
 SQ

Query Match 7.5%; Score 101; DB 2; Length 566;
 Best Local Similarity 18.0%; Pred. No. 0.45; Mismatches 90; Indels 110; Gaps 13;
 Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

QY 5 LVGFARREVVSADSVRCLSLACLNADTFEGECESVMYYPVDAECLNTEDR----LDRP 59
 Db 33 LFSVTRKKQLGAGSIEBAAKCEEDEE--FICRAFOYHSKQOCVIMAENRKSSIIIR 89
 QY 6 DLFVDEHEDTVYILDNNCAGCCEHHWDFDNFKTSGLNDQOFAIAQCYAPYVTOVAVEG 119
 Db 90 DVLFEKK--VYLSCECKTGNGKVRGTMNSKTKNGITCKWST---SPH----- 133
 QY 120 RQLSDELDISFEGLE-----LSECELCTQ----- 144
 Db 134 RPRSPATHSEGLBENYCRNPNDPQGPWCYTDPKRYDYCILEBECMHCSGENY 193
 QY 145 --RLSVTANDPNCKS-----FMYSNLTTS-CVLSDRSPPLGRANLAEP 186
 Db 194 DGKSKRTMSGLEQWDSOPHAGHYIPSKRPPKNNLKNYCRNPDRRLP----- 243
 QY 187 GWTYFESRGVPSFRVPQMLVGFASPVFMENVPVSTMCIDQCTSPPPETQONFVC 241
 Db 244 -W-----CFTDPN-----KRWELCDIP-----RCTTPPSSGPTYQ 275
 SQ

RESULT 15
 AAY02100
 ID AAY02100 standard; protein; 566 AA.
 XX
 AC AAY02100;
 XX
 DT 16-JUL-1999 (first entry)

DE A multifunctional protein of the invention.
 XX

KW Angiostatin; endostatin; interferon; thrombospondin;
 KW anti-interferon-inducible protein; platelet factor 4; anti-angiogenic;
 KW anti-tumour; multifunctional protein; angiogenic-mediated disease; cancer;
 KW diabetic retinopathy; macular degeneration; arthritis;
 KW tumor cell production.
 OS Synthetic.
 OS Homo sapiens.
 PN WO9916889-A1.

Search completed: March 31, 2005, 02:03:03
 Job time : 177 secs

This Page Blank (uspto)

GenCore version 5.1.6
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OM protein - protein search, using sw model
 Run on: March 31, 2005, 01:57:45 ; Search time 43 Seconds

title: US-10-771-708-11
 Perfect score: 1354
 Sequence: 1 EKQKINGPAREEVNSADSVR. PPEPEIQQNFVCKSVWVYIINE 250

scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

searched: 513545 seqs, 7469064 residues

Total number of hits satisfying chosen parameters: 513545

Minimum DB seq length: 0 (without alignments)
 Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents AA:*

1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep: *
 2: /cgn2_6/ptodata/1/iaa/6A_COMB.pep: *
 3: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep: *
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep: *
 6: /cgn2_6/ptodata/1/iaa/backfilesl.pep: *

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query	Match	Length	DB ID	Description
1	117	8.6	342	4	US-09-270-767-32874	Sequence 32874, A
2	116	8.6	790	4	US-09-991-761A-13	Sequence 33129, A
3	113	8.3	256	4	US-09-270-767-33129	Sequence 48346, A
4	113	8.3	256	4	US-09-270-767-48346	Sequence 7, Appl
5	105	7.7	812	4	US-09-991-761A-11	Sequence 11, Appl
6	104	7.7	810	4	US-09-991-761A-11	Sequence 54, Appl
7	101.5	7.5	790	1	US-09-469-4486-54	Sequence 54, Appl
8	101.5	7.5	790	2	US-09-469-658-54	Sequence 1, Appl
9	101	7.5	791	1	US-09-643-219-1	Sequence 1, Appl
10	101	7.5	791	2	US-09-131-995-1	Sequence 1, Appl
11	101	7.5	791	2	US-09-831-0878-1	Sequence 1, Appl
12	101	7.5	791	3	US-09-851-350-1	Sequence 1, Appl
13	101	7.5	791	3	US-09-132-154-1	Sequence 6, Appl
14	101	7.5	791	4	US-09-991-761A-6	Sequence 1, Appl
15	101	7.5	791	4	US-09-924-287A-1	Sequence 1, Appl
16	101	7.5	810	1	US-09-854-603-2	Sequence 2, Appl
17	101	7.5	810	1	US-09-147-00B-29	Sequence 29, Appl
18	101	7.5	810	3	US-09-086-514-1	Sequence 1, Appl
19	101	7.5	810	4	US-09-192-012-5	Sequence 5, Appl
20	101	7.5	810	4	US-09-403-736-1	Sequence 1, Appl
21	101	7.5	810	4	US-09-701-265-1	Sequence 1, Appl
22	101	7.5	810	6	5200340-8	Patent No. 5200340
23	101	7.5	814	1	US-09-750-711-1	Sequence 1, Appl
24	101	7.5	812	1	US-09-248-629A-1	Sequence 1, Appl
25	99	7.3	812	1	US-09-451-932-1	Sequence 1, Appl
26	99	7.3	812	1	US-09-452-260-1	Sequence 1, Appl
27	99	7.3	812	1	US-09-452-260-1	Sequence 1, Appl

RESULT 1
 US-09-270-767-32874
 Sequence 32874, Application US/09270767
 Patent No. 670491

GENERAL INFORMATION:

APPLICANT: Homburger et al.

TITLE OF INVENTION: Nucleic acids and proteins of *Drosophila melanogaster*

FILE REFERENCE: File Reference: 7356-094

CURRENT APPLICATION NUMBER: US/09-270-767

CURRENT FILING DATE: 1999-03-17

NUMBER OF SEQ ID NOS: 62517

SOFTWARE: PatentIn Ver. 2.0

SEQ ID NO: 32874

LENGTH: 342

TYPE: PRT

ORGANISM: *Drosophila melanogaster*

US-09-270-767-32874

Query Match 8.6%; Score 117; DB 4; Length 342;
 Best Local Similarity 23.6%; Pred. No. 0.00023; Mismatches 98; Indels 76; Gaps 15;
 Matches 64; Conservative 33; MisMatch 98; Indels 76; Gaps 15;

QY	3 KILVGFAREVNSADSVR. VRHCLSLACINAFDTFFGFCESVWVYPPVDAECL- 50
Db	36 EILTY--VLSAVSKMLDTLPGTMLTCLEAQN----NESCAVNV--EGLCVLP 85
QY	51 -NTEDRLDRDPLFVDEBHDFTVYDNNCAG--CCEWHWDFDNPKNSGLNDQQFAIAQC 106
Db	86 KTTADKLKP-GSLRSQFPPVFTIYQKSCIGVRPSKAWC1DR----- 126
QY	107 YAPVYTIQVIAVEGQLSDLSDHSFEGLELSECBLCTQRLSVTANDFNCFSMVLNTRS 166
Db	127 -----VQGYRLPEHVKSQSVTLRSRDCBLIC-----LGBTEFTCRSANYRHSGI 171
QY	167 QVLSD-ERSRPLGRNLAEVPGWTFYFESRGV-PS----FTRVQMLVGFASFVNENVP 219
Db	172 CELSDMDRITISAGGSVERYDGADELNNECAERSKLCIFPRKISGKILKIVDS-VHQDIN 230
QY	220 SVTMCILDOCTSPPRBTGONFVCKSVWVYIINE 250
Db	231 TIDCRDLCLNSP-----YRCHS--YDYN 253

RESULT 2
 US-09-991-761A-13
 Sequence 13, Application US/09991761A

Patent No. 6576609

GENERAL INFORMATION:

APPLICANT: Soff, Gerald

ATTORNEY: Gately, Stephen

APPLICANT: Twardowski, Przemyslaw
 TITLE OF INVENTION: "Methods and Compositions for Generating
 TITLE OF INVENTION: Angiooatatin"
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSE: Sheridan Ross P.C.
 STREET: 1700 Lincoln St., Suite 3500
 CITY: Denver
 STATE: CO
 COUNTRY: USA
 ZIP: 80203
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patentin Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/991,761A
 FILING DATE:
 CLASSIFICATION: 1642
 ATTORNEY/AGENT INFORMATION:
 NAME: Crook, Wannell M.
 REFERENCE/DOCKET NUMBER: 31.071
 PREFERENCE/DOCKET NUMBER: 3501-16-1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: (303) 863-9700
 TELEFAX: (303) 863-0223
 INFORMATION FOR SEQ ID NO: 13:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 790 amino acids
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: protein
 US-08-991-761A-13

Query Match 8.6%; Score 116; DB 4; Length 790;
 Best Local Similarity 19.5%; Pred. No. 0 00098; Mismatches 55; Conservatve 43; Indels 100; Gaps 84; Matches 55; Conservative 43; Mismatches 43; Indels 84; Gaps 12;

Qy 5 LVGFAREVVSADSVRCLASACLNAAFDFTGFECESSVMYYPVDAECLNTEDRDRPDLF 64
 Db 14 LsLsLsRQKVaAaSVEECAKc-EAEI-NFICRAQFQHSKQDQCVVNAENSKTSPP--IA 67
 Qy 65 EHDTV-----TLDNNCAGCCEWHFDNFKTSGLNQDQFAIAACQYAPYVQYAVEG 119
 Db 68 RURDVLVLFKRYLSECKTGKNGKRYGRTSKVSKGVIQKWSVSSPHKPSPEKPLAG 127
 Qy 120 RQ-----LSDEDHSEGLESECEBLCTQ-----RUYTANDFNC 155
 Db 128 LEENYCRNPDNDERKGPMWCYTPTETREDYCDIPECEBCMHSGEHYEGKUXTMSGIEC 187
 Qy 156 KS-----FMSNITRS_CVLRSRSRPLGRANLAEVFGWTESRGVSPF 199
 Db 188 QSMGSQSPHAG3YLPSPKNKLMNQYCRNPPGEPFRP-----W-----CF 227
 Qy 200 TRVQMLLVGFASFVMENVPSPVTMCLDOCTSPPETGONFVC 241
 Db 228 TTPN-----KRWPCDIP-----RCTTPTPSTGTYQ 256

US-08-991-761A-13

RESULT 3 ; SEQ ID NO 33129
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; US-09-270-767-48346
 ; Sequence 48346, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; SEQ ID NO 48346
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; US-09-270-767-48346

Query Match 8.3%; Score 113; DB 4; Length 256;
 Best Local Similarity 21.3%; Pred. No. 0 00041; Mismatches 47; Conservatve 28; Indels 64; Gaps 7; Matches 47; Conservatve 28; Mismatches 82; Indels 64; Gaps 7;

Qy 3 KILVGFAREVVSADSVRCLASACLNAAFDFTGFECESSVMYYPVDAECLNTEDRDRPDLF 62
 Db 47 KBRIGLNDNLIYTSTKEACLSACLN--ERRFVCRSVEYDYNMKCVLSDRRSSGQFV 103
 Qy 63 VDEHEDTVILDNNC--ACCECHWHFDNFKTSGLNQDQFAIAACQYAPYVQYAVEG 118
 Db 104 QLVDAGQTDPENLCKPKAACKNRSSFGNSQMGVSEK-----VAQYVGL- 150
 Qy 119 GRLSDELDHSFEGLESECEBLCTQRLSTANDNCKSMNLT-----165
 Db 151 -----KHYTDKELQVTSSEACRLACELESLCRSLVYQGQSQYNCRLYHLDH 201

Qy 166 -----SCVLSDER---SRPLGRANLAEVFGWTESRGVSPF 194
 Db 202 KTLPDGPSTYLNHERPLDGEPIGO-----YFENQ 232

RESULT 5 ; SEQ ID NO 33129
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; US-09-270-767-33129
 ; Sequence 33129, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Homburger et al.
 ; TITLE OF INVENTION: Nucleic acids and proteins of Drosophila melanogaster
 ; FILE REFERENCE: File Reference: 7326-094
 ; CURRENT APPLICATION NUMBER: US/09/270,767
 ; CURRENT FILING DATE: 1999-03-17
 ; NUMBER OF SEQ ID NOS: 62517
 ; SOFTWARE: Patentin Ver. 2.0

RESULT 5 ; SEQ ID NO 33129
 ; LENGTH: 256
 ; TYPE: PRT
 ; ORGANISM: Drosophila melanogaster
 ; US-09-270-767-33129
 ; Sequence 33129, Application US/09270767
 ; Patent No. 6703491
 ; GENERAL INFORMATION:
 ; APPLICANT: Soft, Gerald
 ; APPLICANT: Gately, Stephen

APPLICANT: Twardowski, Przemyslaw
TITLE OF INVENTION: "Methods and Compositions for Generating
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:
ADDRESSEE: Sheridan Ross P.C.
STREET: 1700 Lincoln St., Suite 3500
CITY: Denver
STATE: CO
COUNTRY: USA
ZIP: 80203

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/991,761A
FILING DATE:
CLASSIFICATION: 1642
ATTORNEY/AGENT INFORMATION:
NAME: Crook, Wannell M.
REGISTRATION NUMBER: 31,071
REFERENCE/DOCKET NUMBER: 3501-16-1
TELECOMMUNICATION INFORMATION:
TELEPHONE: (303) 863-9700
TELEFAX: (303) 863-0223
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
LENGTH: 810 amino acids
TYPE: amino acid
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: protein
US-08-991-761A-7

Query Match 7.8%; Score 105; DB 4; Length 812;
Best Local Similarity 18.3%; Pred. No. 0.01%;
Matches 55; Conservative 42; Mismatches 83; Indels 120; Gaps 17;
Matches 55; Conservative 38; Mismatches 89; Indels 118; Gaps 14;
Matches 54; Conservative 38; Mismatches 89; Indels 118; Gaps 14;

Qy 5 LVGPREVVSADSVRCLSLACLNAAFDTFGFCESVMYPPVDAECLNTEDRLDRDPLFVD 64
Db 33 LPSTTKQAGGSFECANKCEREE--FICRSFQHAKQEQQVIMAE--NRKSSIVP 86
Qy 65 EHEDTVIYLN--NC--AGCCEH-W---HEDNPKTSGILNDQ 98
Db 64 RMRDVLYKEKRYLBLECKTGNGQTYRGTTABTKSGVTCQMSATSPHPKF----SPE 147
Qy 87 RMRDVLYF-----EKVYLSBCKTGNGKNYRTGMSKRTGTCQWSSTSPPH----- 133
Db 99 QPAIAA--QCYAP-----YTTQYVAVEGQLQLSBDLHSFEGGLESECBELCTQ- 144
Qy 116 AVEGQLSBDLHSFEGGLESECBELCTQ-----LSECBELCTQ- 144
Db 134 ----RPTFSATHSSEGLBNENYCRNPDPNDGQGPWCVYTDPEERFDYCIPEDBCMICS 189
Qy 145 -----RLSFTANDPNCK-----FMYSNLTRS-CVLSDERSRPLGRANL 182
Db 190 GENYDGKISKIMSGLQCAWDSQSPHAGYIPLSPKPNKNUKKNYCRNPDPGEPRP----- 243
Qy 183 AEVPGWTFESRGVFFTRVPQMLLVGASFVVMENPVSVTMCLDQCTSPPPETQNFVC 241
Db 244 -----W-----CFTTDPN-----KRWELCDIP-----RCTTPPPSSGPTYQC 275

RESULT 7
US-08-469-486-54
; Sequence 54, Application US/08469486
; Patent No. 573981
; GENERAL INFORMATION:
; APPLICANT: Thoegersen, Hans Christian
; APPLICANT: Holtet, Thor, Lars
; APPLICANT: Ezerot, Michael
; TITLE OF INVENTION: Improved method for the refolding of
; proteins
; NUMBER OF SEQUENCES: 58
; CORRESPONDENCE ADDRESS:
; ADDRESSEE: Fish & Richardson
; STREET: 225 Franklin Street
; CITY: Boston
; STATE: Massachusetts
; COUNTRY: USA
SUIT 6
-08-991-761A-11
Sequence 11, Application US/08991761A
PATENT NO. 6576609
GENERAL INFORMATION:
APPLICANT: Soft, Gerald
APPLICANT: Gately, Stephen
APPLICANT: Twardowski, Przemyslaw
TITLE OF INVENTION: "Methods and Compositions for Generating
TITLE OF INVENTION: "Methods and Compositions for Generating
NUMBER OF SEQUENCES: 16
CORRESPONDENCE ADDRESS:

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 2.0

CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/643,219
 FILING DATE: 06-MAY-1996
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER:
 ATTORNEY/AGENT INFORMATION:
 NAME: Casuto, Diane
 REGISTRATION NUMBER: 40,943
 REFERENCE/DOCKET NUMBER: 5940.US.PI

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847-938-3137
 TELEFAX: 847-938-2623
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 791 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE:
 DESCRIPTION: protein

US-08-643-219-1

Query Match 7.5% Score 101; DB 1; Length 791;
 Best Local Similarity 18.0%; Pred. No. 0.045; Mismatches 90; Indels 110; Gaps 13;
 Matches 53; Conservative 42; MisMatches 90; Indels 110; Gaps 13;

QY 5 LVGFAREVVSAADVRLSACLNADFTGFCFCEESVMYVPAECLNTEDR---LDRP 59
 Db 14 LFSVTKKQLAGSSTEECAKCEEDEE--FTCRAQHYSKEQQVIMANRKSSIIIR 70

QY 60 DLFVDEHEPTVILYLDNNCAGCCEHHFDNPKTSGLINDQFAIAQCYAPVYQVAVEG 119
 Db 71 DVLFEKK---VYLSCKTGNKGNYRGTMKTNKGITCQKWSST---SPH----- 114

QY 120 RQLSBDLHSFEGLE-----LSECBELCTQ----- 144
 Db 115 RPRFSPATHPSEGLENVYCRNPDPQGWCYTDPKPKYDQDILECEECMHCSGENY 174

QY 145 --RLSVTANDFNCKS-----FMYSLTRS-CVLSDERSRPLGRANLAEV 186
 Db 175 DGKLSKTMGSLCQWDSDQSPHANGYIPSKFPNKNLKGNYCRNPDRKLAP----- 224

QY 187 GWTYFESRGVPSTRVQMLLVGFASFVMENVPSVTMCLDQCTSPPERGQNFC 241
 Db 225 -W-----CFTDPN---KRWELCDIP-----RCTTPPSSGPTYQC 256

RESULT 10
 US-09-131-995-1
 ; Sequence 1, Application US/09131995
 ; Patent No. 5972896
 ; GENERAL INFORMATION:
 ; APPLICANT: Davidson, Donald J.
 ; TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
 ; TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
 ; NUMBER OF INVENTIONS: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Abbott Laboratories
 ; ADDRESS: Abbott Laboratories
 ; STREET: 100 Abbott Park Road
 ; CITY: Abbott Park
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60064
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS

OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/832,087
 FILING DATE: 03-APR-1997
 APPLICATION NUMBER: 08/643,219
 FILING DATE: 06-MAY-1996

PRIOR APPLICATION DATA:
 APPLICATION NUMBER: 40,943
 REGISTRATION NUMBER: 40,943
 REFERENCE/DOCKET NUMBER: 5940.US.PI

TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847-938-3137
 TELEFAX: 847-938-2623
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 791 amino acids
 TYPE: amino acid
 TOPOLOGY: linear
 MOLECULE TYPE:
 DESCRIPTION: protein

US-09-131-995-1

Query Match 7.5% Score 101; DB 2; Length 791;
 Best Local Similarity 18.0%; Pred. No. 0.045; Mismatches 90; Indels 110; Gaps 13;
 Matches 53; Conservative 42; MisMatches 90; Indels 110; Gaps 13;

QY 5 LVGFAREVVSAADVRLSACLNADFTGFCFCEESVMYVPAECLNTEDR---LDRP 59
 Db 14 LFSVTKKQLAGSSTEECAKCEEDEE--FTCRAQHYSKEQQVIMANRKSSIIIR 70

QY 60 DLFVDEHEPTVILYLDNNCAGCCEHHFDNPKTSGLINDQFAIAQCYAPVYQVAVEG 119
 Db 71 DVLFEKK---VYLSCKTGNKGNYRGTMKTNKGITCQKWSST---SPH----- 114

QY 120 RQLSBDLHSFEGLE-----LSECBELCTQ----- 144
 Db 115 RPRFSPATHPSEGLENVYCRNPDPQGWCYTDPKPKYDQDILECEECMHCSGENY 174

QY 145 --RLSVTANDFNCKS-----FMYSLTRS-CVLSDERSRPLGRANLAEV 186
 Db 175 DGKLSKTMGSLCQWDSDQSPHANGYIPSKFPNKNLKGNYCRNPDRKLAP----- 224

QY 187 GWTYFESRGVPSTRVQMLLVGFASFVMENVPSVTMCLDQCTSPPERGQNFC 241
 Db 225 -W-----CFTDPN---KRWELCDIP-----RCTTPPSSGPTYQC 256

RESULT 11
 US-08-832-087B-1
 ; Sequence 1, Application US/08832087B
 ; Patent No. 598184
 ; GENERAL INFORMATION:
 ; APPLICANT: Davidson, Donald J.
 ; TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
 ; TITLE OF INVENTION: AND METHODS FOR INHIBITING ANGIOGENESIS
 ; NUMBER OF SEQUENCES: 14
 ; CORRESPONDENCE ADDRESS:
 ; ADDRESSEE: Abbott Laboratories
 ; STREET: 100 Abbott Park Road
 ; CITY: Abbott Park
 ; STATE: IL
 ; COUNTRY: USA
 ; ZIP: 60064
 ; COMPUTER READABLE FORM:
 ; MEDIUM TYPE: Diskette
 ; COMPUTER: IBM Compatible
 ; OPERATING SYSTEM: DOS

APPLICATION NUMBER: US/08/851,350
 CURRENT APPLICATION DATA:
 FILING DATE: 05-MAY-1997
 APPLICATION NUMBER: US/08/832,087B
 FILING DATE: 03-APR-1997
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 APPLICATION NUMBER: 08/643,219
 FILING DATE: 06-MAY-1996
 ATTORNEY/AGENT INFORMATION:
 NAME: Casuto, Dianne
 REGISTRATION NUMBER: 40,943
 REFERENCE/DOCKET NUMBER: 5940.US.P1
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847-938-3137
 TELEFAX: 847-938-2623
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 791 amino acids
 TOPology: linear
 MOLECULE TYPE:
 DESCRIPTION: protein
 US-08-832-087B-1

Query Match 7.5%; Score 101; DB 2; Length 791;
 Best Local Similarity 18.0%; Pred. No. 0 045; Mismatches 90; Indels 110; Gaps 13;
 Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;
 Qy 5 LVGFAREVVSADSVRCLASACINAFAADFPGFECESVMVYPVDAECLNTEDR----LDRP 59
 Db 14 LFSVTKKOLGAGSIEECAKCKRDEE--FTCRAQHYSKEQCVIMAENRKSSIIIRMR 70
 Qy 60 DLFDVDEHDIVTYLDDNCAGCCHWHFDNFKTSGLNDQFAIAAQCYAPVYQVAVEG 119
 Db 71 DVLFLERKK--VYLSCKTGNGKNGYRGTMSKTKNGITCOKNST---SPH----- 114
 Qy 120 RQLSDELDHSFEGLE-----LSECEELCTQ----- 144
 Db 115 RPRFSPATHPSIGEGLBENYCRNPDPQGPWCYTIDPEKRYDYLCEECMHCSGENY 174
 Qy 145 -RLSVTANDFNCKS-----FMYSNLTRS-CVLSDERSRPLGRANIAEV 186
 Db 175 DGKISKIMSGLQCAWDSQSPHAGYIIPSKFPKNLKQVNCNPDRLRP----- 224
 Qy 187 GWTYFESRGVPSFTRVPOMLVGFASPYMENVPSTMCLQDTSPPETGQFVC 241
 Db 225 -W-----CFTDPN-----KRWECLDIP-----RCTIPPPSSGPTYQC 256

RESULT 12
 US-08-851-350-1
 Sequence 1, Application US/08851350
 Patent No. 6057122
 GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories
 TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES, AND METHODS
 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME, AND METHODS
 TITLE OF INVENTION: FOR INHIBITING ANGIOGENESIS
 NUMBER OF SEQUENCES: 38
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064-3500
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/132,154
 FILING DATE:
 CLASSIFICATION:

APPLICATION NUMBER: US/08/851,350
 CURRENT APPLICATION DATA:
 FILING DATE: 05-MAY-1997
 CLASSIFICATION: 514
 PRIORITY APPLICATION DATA:
 ATTORNEY/AGENT INFORMATION:
 NAME: Casuto, Dianne
 REGISTRATION NUMBER: 40,943
 REFERENCE/DOCKET NUMBER: 5940.US.P2
 TELECOMMUNICATION INFORMATION:
 TELEPHONE: 847-938-3137
 TELEFAX: 847-938-2623
 TELEX:
 INFORMATION FOR SEQ ID NO: 1:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 791 amino acids
 TYPE: amino acid
 TOPology: linear
 MOLECULE TYPE:
 DESCRIPTION: protein
 US-08-851-350-1

Query Match 7.5%; Score 101; DB 3; Length 791;
 Best Local Similarity 18.0%; Pred. No. 0.045; Mismatches 90; Indels 110; Gaps 13;
 Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;
 Qy 5 LVGFAREVVSADSVRCLASACINAFAADFPGFECESVMVYPVDAECLNTEDR----LDRP 59
 Db 14 LFSVTKKOLGAGSIEECAKCKRDEE--FTCRAQHYSKEQCVIMAENRKSSIIIRMR 70
 Qy 60 DLFDVDEHDIVTYLDDNCAGCCHWHFDNFKTSGLNDQFAIAAQCYAPVYQVAVEG 119
 Db 71 DVLFLERKK--VYLSCKTGNGKNGYRGTMSKTKNGITCOKNST---SPH----- 114
 Qy 120 RQLSDELDHSFEGLE-----LSECEELCTQ----- 144
 Db 115 RPRFSPATHPSIGEGLBENYCRNPDPQGPWCYTIDPEKRYDYLCEECMHCSGENY 174
 Qy 145 -RLSVTANDFNCKS-----FMYSNLTRS-CVLSDERSRPLGRANIAEV 186
 Db 175 DGKISKIMSGLQCAWDSQSPHAGYIIPSKFPKNLKQVNCNPDRLRP----- 224
 Qy 187 GWTYFESRGVPSFTRVPOMLVGFASPYMENVPSTMCLQDTSPPETGQFVC 241
 Db 225 -W-----CFTDPN-----KRWECLDIP-----RCTIPPPSSGPTYQC 256

RESULT 13
 US-09-132-154-1
 Sequence 1, Application US/09132154
 Patent No. 6251867
 GENERAL INFORMATION:
 APPLICANT: Davidson, Donald J.
 TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES
 NUMBER OF SEQUENCES: 14
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Abbott Laboratories
 STREET: 100 Abbott Park Road
 CITY: Abbott Park
 STATE: IL
 COUNTRY: USA
 ZIP: 60064
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette
 COMPUTER: IBM Compatible
 OPERATING SYSTEM: DOS
 SOFTWARE: FastSEQ Version 2.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/09/132,154
 FILING DATE:
 CLASSIFICATION:

PRIORITY APPLICATION DATA:

APPLICATION NUMBER: US/08/832,087

FILING DATE: 03-APR-1997

APPLICATION NUMBER: 08/643,219

FILING DATE: 06-MAY-1996

ATTORNEY/AGENT INFORMATION:

NAME: Casuto, Diane

REGISTRATION NUMBER: 40,943

REFERENCE/DOCKET NUMBER: 5940.US.P1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 791 amino acids

TOPeOY: 847-938-3137

TELEFAX: 847-938-2623

INFORMATION FOR SEQ ID NO: 1:

SEQUENCE CHARACTERISTICS:

LENGTH: 791 amino acids

TOPeOY: amino acid

MOLECULE TYPE: linear

DESCRIPTION: protein

US-09-132-154-1

Query Match 7.5%; Score 101; DB 3; Length 791;
 Best Local Similarity 18.0%; Pred. No. 0.045; M1 matches 90; Indels 110; Gaps 13;
 Matches 53; Conservative 42; Mismatches 90; Delins 110; Gaps 13;

Query 5 LVGFAREVVSADSVRCLSLACLNAAFDTCFECESVMMVPPVDACTLNEDR----LDRP 59
 Db 14 LFSVTRKKQLGAGSIEBAAKCEEDER--FTCRAFOYHSKQOCVIMAENRKSSIIIRMR 70

Query 60 DLFVBDHEDTVILDNNCAGCEHHFDNFKTSGLNDQFAIAAQCYAPIVQYAVEG 119
 Db 71 DVVLFEKK--VYLSCECKTGNGKVRGTMSTKNGTICKQWST---SPH----- 114

Query 120 RQLSDELDHSFEGLE-----LSECBELCTO----- 144
 Db 115 RPRFSPATHSEGLENVYCRNPNDPQGPWCYTDPKEKRYDQILEBECMCMSGENV 174

Query 145 --RISVTAENDNC-----FWMNSNLTS-CVNSDERSRPLGRANLAEVP 186
 Db 175 DGKISKTMMSGLECQAWDSQSOPHAGYIPSKRFPNKNLKKQYCRNPDRRLRP----- 224

Query 187 GWTYFESRGVPSFTRVQMLVGFASFVMEVNPVSTMCLDQCTSPPPERGQNFCV 241
 Db 225 -W-----CFTTDPN----KRWELCDIP-----RCTTPPSSGPTYOC 256

RESULT 14
 US-08-991-761A-6
 Sequence 6, Application US/08991761A
 Patent No. 6576609
 GENERAL INFORMATION:
 APPLICANT: Sofi, Gerald
 APPLICANT: Gately, Stephen
 APPLICANT: Twardowski, Przemyslaw
 TITLE OF INVENTION: "Methods and Compositions for Generating
 NUMBER OF SEQUENCES: 16
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Sheridan Ross P.C.
 STREET: 1700 Lincoln St., Suite 3500
 CITY: Denver
 STATE: CO
 COUNTRY: USA
 ZIP: 80203

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: PatentIn Release #1.0, Version #1.30
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/991-761A
 FILING DATE:

CLASSIFICATION: 1642

ATTORNEY/AGENT INFORMATION:

NAME: Crock, Wannell M.

REGISTRATION NUMBER: 31,071

REFERENCE/DOCKET NUMBER: 3501-16-1

TELECOMMUNICATION INFORMATION:

TELEPHONE: (303) 863-9700

TELEFAX: (303) 863-0223

INFORMATION FOR SEQ ID NO: 6:

SEQUENCE CHARACTERISTICS:

LENGTH: 791 amino acids

TYPE: amino acid

STRANDEDNESS: single

TOPeOY: linear

MOLECULE TYPE: protein

US-08-991-761A-6

Query Match 7.5%; Score 101; DB 4; Length 791;
 Best Local Similarity 18.0%; Pred. No. 0.045; M1 matches 90; Indels 110; Gaps 13;
 Matches 53; Conservative 42; Mismatches 90; Delins 110; Gaps 13;

Query 5 LVGFAREVVSADSVRCLSLACLNAAFDTCFECESVMMVPPVDACTLNEDR----LDRP 59
 Db 14 LFSVTRKKQLGAGSIEBAAKCEEDER--FTCRAFOYHSKQOCVIMAENRKSSIIIRMR 70

Query 60 DLFVBDHEDTVILDNNCAGCEHHFDNFKTSGLNDQFAIAAQCYAPIVQYAVEG 119
 Db 71 DVVLFEKK--VYLSCECKTGNGKVRGTMSTKNGTICKQWST---SPH----- 114

Query 120 RQLSDELDHSFEGLE-----LSECBELCTO----- 144
 Db 115 RPRFSPATHSEGLENVYCRNPNDPQGPWCYTDPKEKRYDQILEBECMCMSGENV 174

Query 145 --RISVTAENDNC-----FWMNSNLTS-CVNSDERSRPLGRANLAEVP 186
 Db 175 DGKISKTMMSGLECQAWDSQSOPHAGYIPSKRFPNKNLKKQYCRNPDRRLRP----- 224

Query 187 GWTYFESRGVPSFTRVQMLVGFASFVMEVNPVSTMCLDQCTSPPPERGQNFCV 241
 Db 225 -W-----CFTTDPN----KRWELCDIP-----RCTTPPSSGPTYOC 256

RESULT 15
 US-08-924-287A-1
 Sequence 1, Application US/08924287A
 Patent No. 669938
 GENERAL INFORMATION:
 APPLICANT: Abbott Laboratories

APPLICANT: Davidson, Donald J.
 TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES, AND METHODS FOR INHIBITING
 TITLE OF INVENTION: POLYNUCLEOTIDES ENCODING SAME, AND METHODS FOR INHIBITING
 FILE REFERENCE: 5940.US.P3
 CURRENT APPLICATION NUMBER: US/08/924,287A
 CURRENT FILING DATE: 1997-09-05
 PRIOR APPLICATION NUMBER: US 08/851,350
 PRIOR FILING DATE: 1997-05-05
 PRIOR APPLICATION NUMBER: US 08/832,087
 PRIOR FILING DATE: 1997-04-03
 PRIOR APPLICATION NUMBER: US 08/643,219
 PRIOR FILING DATE: 1996-05-03
 NUMBER OF SEQ ID NOS: 40
 SOFTWARE: FastSBQ for Windows Version 4.0
 SEQ ID NO: 1
 LENGTH: 791
 TYPE: PRT
 ORGANISM: Homo sapiens
 US-08-924-287A-1

Query Match 7.5%; Score 101; DB 4; Length 791;
 Best Local Similarity 18.0%; Pred. No. 0.045; M1 matches 90; Indels 110; Gaps 13;

QY	5	LVGFKEEVNSADSVRVCILSACINAAFPFGFRCESVMMYTPVDAECLNTEDR-----LDRP 59
Db	14	LFSVYTKQLGAGSITBCAAKCEEDER----FTCRAFOHSKEQOQVIMAENRKSIIIRMR 70
QY	60	DLFVDEHEDTVIYLDNNCAGCECHWIFDNFKTSGLNDQFAIAQCYAPVYQVAVEG 119
Db	71	DWVLEKK---VYLSBCKTGKNGKNTGTMKSKTNGKGTICQKWSST-----SPH----- 114
QY	120	RQLSFLDHSPEGLE----- 144
Db	115	RPRISPATHSEGGLEBNYCRNPNDPQGPWCYTTFBKRYDCCLEEECHMCHEGENY 174
QY	145	--RUYVTAENDPNCKS-----FMYNLTNTS-CVTLSDRSRSPRGLRANLAEPV 186
Db	175	DGKVSKTMSGLECQWDSQSPHAHYIIPSKRPNKNUJKKNYCRNPDRBLRP----- 224
QY	187	GWTTEFESRGAPSFTVQPMQLINGFASFVUMENPVSPVWMLDCTSPPETGOFVC 241
Db	225	-W-----CFTTDN-----KREWELCDIP-----RCTTPPPSSGPTYQC 256

Search completed: March 31, 2005, 02:07:44
Job time : 44 secs

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OM protein - protein search, using sw model

Run on: March 31, 2005, 02:00:10 ; Search time 140 Seconds
(without alignments)
591.252 Million cell updates/sec

Title: US-10-771-708-11
Perfect score: 1354
Sequence: 1 BQKILVGFAREVVSADSVHR..... PPPETGQNFFVCKSVMYYNE 250

Scoring table: BLOSUM62
Searched: Gapop 10.0 , Gapext. 0.5

Total number of hits satisfying chosen parameters: 1407402
Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Listing first 45 summaries

Database : Published Applications AA:*

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- 2: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US10_PUBCOMB.pep:*
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- 17: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_PUBCOMB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUBCOMB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Query %
Match Length DB ID Description

Result No. Score Match Length DB ID Description

1 116 8.6 790 10 US-09-825-751A-70 Sequence 70, Appli

2 105 7.8 812 10 US-09-825-751A-71 Sequence 71, Appli

3 101 7.5 816 10 US-10-741-601-413 Sequence 413, Appli

4 101 7.5 569 9 US-09-946-893-5 Sequence 5, Appli

5 101 7.5 571 9 US-09-946-893-8 Sequence 1, Appli

6 101 7.5 576 9 US-09-946-893-6 Sequence 6, Appli

7 101 7.5 791 9 US-09-967-386-1 Sequence 1, Appli

8 101 7.5 791 14 US-10-304-287-1 Sequence 1, Appli

9 101 7.5 791 15 US-10-360-101-257 Sequence 257, Appli

10 101 7.5 791 16 US-10-778-423-1 Sequence 1, Appli

11 101 7.5 791 16 US-10-753-646-1 Sequence 1, Appli

12 101 7.5 791 16 US-10-735-557-7 Sequence 1, Appli

13 101 7.5 810 9 US-09-946-893-2 Sequence 2, Appli

SUMMARIES

RESULTS

RESULT 1
US-09-825-751A-70

; Sequence 70, Application US/09925751A
; Publication No. US20030065140A1

; GENERAL INFORMATION:

; APPLICANT: Curagen Corporation

; APPLICANT: Vernet, Corine A.M.

; APPLICANT: Fernandes, Elma R.

; APPLICANT: Taurier, Raymond J

; APPLICANT: Quinn, Kerry E

; APPLICANT: Sporek, Kimberly A

; APPLICANT: Rastelli, Luca

; APPLICANT: Herman, John L

; TITLE OF INVENTION: Novel Proteins and Nucleic Acids Encoding Same

; FILE REFERENCE: 15966-750

; CURRENT APPLICATION NUMBER: US/09/825,751A

; PRIORITY FILING DATE: 2001-04-30

; PRIORITY NUMBER: 60/194,314

; NUMBER OF SEQ ID NOS: 85

; SOFTWARE: PatentIn Ver. 2.1

; SEQ ID NO 70

; LENGTH: 790

; TYPE: PRT

; ORGANISM: Sub scrofa

; US-09-825-751A-70

Query Match Score 8.6%; Length 790;

Best Local Similarity 19.5%; Pred. No. 0.0064;

Matches 55; Conservative 43; Mismatches 100; Indels 84; Gaps 12;

Qy 5 LVGFAREVVSADSVHRCLACLNADTDFQFPECESMVYVDAECLNLNTDRDLPDFD 64

Db 14 LFLSLRKQVAARSVECAAKC--EAET-NPICRAFQHNSKDDQQCVVAMANSKTSPP--IA 67

QY 65 EHEPTV----IVDNNCAGCECHWHDNFKTSQGILINDQQFATAAQCYAPYVQVAVEG 119
; Sequence 413, Application US/10741601
; Publication No. US200401166519A1
; GENERAL INFORMATION:
; APPLICANT: CARGILL, Michele et al.
; TITLE OF INVENTION: GENETIC POLYMORPHISMS ASSOCIATED WITH
; TITLE OF INVENTION: STENOSIS, METHODS OF DETECTION AND USES THEREOF
; FILE REFERENCE: CL001500
; CURRENT APPLICATION NUMBER: US/10/741,601
; CURRENT FILING DATE: 2003-12-22
; NUMBER OF SEQ ID NOS: 26415
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 413
; LENGTH: 567
; TYPE: PRT
; ORGANISM: Homo sapiens
; US-10-741-601-413
; Query Match 7,5%; Score 101; DB 16; Length 567;
; Best Local Similarity 18,0%; Pred. No. 0,16;
; Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;
; QY 5 LVGFAREVVSAHSVRLCASICLNAFDTGFPECESSVYVYPDAECLNTEDR----LDRP 59
; Db 33 LSVVKQLGSISBEECAACEBEE----FTCRAQHQSKEOQCUMARNSLILRK 89
; QY 60 DLFVDFHEDPTVYLQDNNCAGCECHWHDNFKTSQGILINDQQFATAAQCYAPYVQVAVEG 119
; Db 90 DVLFEEKK--VYLSBCKTNGKNGTWSKTKNGITCQWST----SPH---- 133
; QY 120 RQSLDLDASFEGLE----LSECEBLCTQ---- 144
; Db 134 RPRFSPATHSEGLELVENNCAGCECHWHDNFKTSQGILINDQQFATAAQCYAPYVQVAVEG 193
; QY 145 --RLSVTANDFNCKS----FMYSNLTRS--CVLSDRSRPLGRANLAEV 186
; Db 194 DKISKITMSGIECQWDSQSPHANQYIPSKFENPKLAKVYCRNDFRELP---- 243
; PRIOR APPLICATION NUMBER: 60/194,314
; PRIOR FILING DATE: 2000-04-03
; PRIORITY NUMBER: 194,314
; PRIORITY APPLICATION NUMBER: 60/225,693
; PRIORITY FILING DATE: 2000-08-16
; NUMBER OF SEQ ID NOS: 85
; SOFTWARE: Patentin Ver. 2.1
; SEQ ID NO: 71
; LENGTH: 812
; TYPE: PRT
; ORGANISM: Bos taurus
; US-09-825-751A-71
; Query Match 7,8%; Score 105; DB 10; Length 812;
; Best Local Similarity 18,3%; Score 105; DB 10; Length 812;
; Matches 55; Conservative 42; Mismatches 83; Indels 120; Gaps 17;
; QY 5 LVGFAREVVSAHSVRLCASICLNAFDTGFPECESSVYVYPDAECLNTEDR----LDRP 64
; Db 40 LSLSLRKLQLAGRSVDECAAKCBEETD--FVGRAFQHSKEQCQCVMAENSKNTP--VF 93
; QY 65 EHEDTIVYLDN----NC----AGCCH-W----HFDNFKTSQGILINDQ 98
; Db 94 RMRDVILYERKRYLLEBECKTNGOTYRGTAETKSGVTCQKNSATSHPVPKF----SPE 147
; QY 99 QFQIAA----QCYAP----YVQYQVAVEGRQLSDELDHSFPEGLSRECEBLCTQ- 144
; Db 148 KFPLAGLBNYCRNPDNDENGFWCYTT----DPDKRYCDIPCECDKMC 195
; QY 145 ----RLSFTANDFNCKS----FMYSNLTRS--CVLSDRSRPLGRAN 181
; Db 196 SGENYEGKIAKIMSGRQCQAMWSQSPHAGYIPSKFENPKLAKVYCRNDFRELP---- 250
; QY 182 LAEVPGWNTYFESRGVPSFTRVQMLVGFASFVMENVPSVTCMLDOCTSPPRETEGONFVC 241
; Db 251 ----W----CFTTDQ----KRWEFCDIP----RCTIPPPSSGKYQC 282
; Query Match 7,5%; Score 101; DB 9; Length 569;
; Best Local Similarity 18,0%; Pred. No. 0,16;
; Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;
; QY 5 LVGFAREVVSAHSVRLCASICLNAFDTGFPECESSVYVYPDAECLNTEDR----LDRP 59
;

RESULT 5
 US-09-946-893-8
 ; Sequence 8, Application US/09946893
 ; Patent No. US20020072494A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yihai
 ; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
 ; TITLE OF INVENTION: Inhibitors
 ; FILE REFERENCE: Mewburn
 ; CURRENT APPLICATION NUMBER: US/09/946,893
 ; CURRENT FILING DATE: 2001-09-05
 ; PRIORITY APPLICATION NUMBER: US 60/230,893
 ; PRIORITY FILING DATE: 2000-09-05
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 576
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Angioquiescin
 ; OTHER INFORMATION: with a tumor targeting signal
 ; US-09-946-893-6

Query Match 7.5%; Score 101; DB 9; Length 576;
 Best Local Similarity 18.0%; Pred. No. 0.16; Matches 53; Conservatve 42; Mismatches 90; Indels 110; Gaps 13;

Query 5 LVGFAREVVSAADVRCCLSACLNADFDFGFECESMVYVYDAACTLNTRD----LDRP 59
 Db 33 LFSVTKQGAGSIEECAKCEDEE--FTCRAFOYHSKEQQCVIMAENRKSSIIIRR 89
 Query 60 DLFVDEHEDTVIYLDNNCAGCEHHWFDFNFKTSGLNDQFAIAQCYAPYVQYAVEG 119
 Db 90 DVVLFEKK---VVLSECKTGNGKNGYRGTMSKTKNGITCOKWST---SPH---- 133
 ; CURRENT FILING DATE: 2001-09-05
 ; PRIORITY APPLICATION NUMBER: US 60/230,893
 ; PRIORITY FILING DATE: 2000-09-05
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 571
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Angioquiescin
 ; OTHER INFORMATION: with a tumor targeting signal peptide
 ; US-09-946-893-8

RESULT 5
 US-09-946-893-8
 ; Sequence 8, Application US/09946893
 ; Patent No. US20020072494A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yihai
 ; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth
 ; TITLE OF INVENTION: Inhibitors
 ; FILE REFERENCE: Mewburn
 ; CURRENT APPLICATION NUMBER: US/09/946,893
 ; CURRENT FILING DATE: 2001-09-05
 ; PRIORITY APPLICATION NUMBER: US 60/230,893
 ; PRIORITY FILING DATE: 2000-09-05
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 576
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Angioquiescin
 ; OTHER INFORMATION: with a tumor targeting signal
 ; US-09-946-893-6

Query Match 7.5%; Score 101; DB 9; Length 576;
 Best Local Similarity 18.0%; Pred. No. 0.16; Matches 53; Conservatve 42; Mismatches 90; Indels 110; Gaps 13;

Query 5 LVGFAREVVSAADVRCCLSACLNADFDFGFECESMVYVYDAACTLNTRD----LDRP 59
 Db 33 LFSVTKQGAGSIEECAKCEDEE--FTCRAFOYHSKEQQCVIMAENRKSSIIIRR 89
 Query 60 DLFVDEHEDTVIYLDNNCAGCEHHWFDFNFKTSGLNDQFAIAQCYAPYVQYAVEG 119
 Db 90 DVVLFEKK---VVLSECKTGNGKNGYRGTMSKTKNGITCOKWST---SPH---- 133
 ; CURRENT FILING DATE: 2001-09-05
 ; PRIORITY APPLICATION NUMBER: US 60/230,893
 ; PRIORITY FILING DATE: 2000-09-05
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 8
 ; LENGTH: 571
 ; TYPE: PRT
 ; ORGANISM: Artificial Sequence
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Angioquiescin
 ; OTHER INFORMATION: with a tumor targeting signal peptide
 ; US-09-946-893-8

RESULT 7
 US-09-967-386-1
 ; Sequence 1, Application US/09967386
 ; Patent No. US2002015992A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; APPLICANT: Henkin, Jack
 ; APPLICANT: Davidson, Donald J.
 ; TITLE OF INVENTION: ANTIANGIOGENIC POLYPEPTIDES AND METHODS
 ; TITLE OF INVENTION: FOR INHIBITING ANGIOGENESIS
 ; FILE REFERENCE: 6730.US.02
 ; CURRENT APPLICATION NUMBER: US/09/967,386
 ; CURRENT FILING DATE: 2001-09-26
 ; PRIORITY APPLICATION NUMBER: US 60/236,550
 ; PRIORITY FILING DATE: 2000-09-29
 ; NUMBER OF SEQ ID NOS: 7
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 791
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-967-386-1

Query Match 7.5%; Score 101; DB 9; Length 791;
 Best Local Similarity 18.0%; Pred. No. 0.24; Matches 53; Conservatve 42; Mismatches 90; Indels 110; Gaps 13;

Query 5 LVGFAREVVSAADVRCCLSACLNADFDFGFECESMVYVYDAACTLNTRD----LDRP 59
 Db 14 LFSVTKQGAGSIEECAKCEDEE--FTCRAFOYHSKEQQCVIMAENRKSSIIIRR 70
 ; CURRENT APPLICATION NUMBER: US 60/230,893
 ; PRIORITY APPLICATION NUMBER: US 60/230,893
 ; PRIORITY FILING DATE: 2000-09-05
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 6
 ; LENGTH: 576
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; FEATURE:
 ; OTHER INFORMATION: Description of Artificial Sequence: Angioquiescin
 ; OTHER INFORMATION: with a tumor targeting signal
 ; US-09-967-386-1

RESULT 6
 US-09-946-893-6
 ; Sequence 6, Application US/09946893
 ; Patent No. US20020072494A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yihai

QY 60 DLFVDEHEDTVYLDNNCAGCCECHWHDNFNKTSGLINDQOFAIAQCYAPVTVQVAVEG 119 ; CURRENT APPLICATION NUMBER: US 10/360,101
; PRIORITY: 2003-02-07
; PRIORITY NUMBER: EP 02077050.8
; PRIORITY FILING DATE: 2002-05-24
; NUMBER OF SEQ ID NOS: 309
; SOFTWARE: Patentin version 3.1
; SEQ ID NO: 257
; LENGTH: 791
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: sequence of plasminogen

Db 115 RPRSPATHPSGLEENYCRNPDNDPQGPWCYTDPKRYDYLCEECMHCSGENY 174 ;
; LENGTH: 791
; TYPE: PRT
; ORGANISM: Artifical Sequence
; FEATURE: OTHER INFORMATION: sequence of plasminogen

QY 145 -RLSVTANDFCKS-----FMYSNLRS-CVLSDDRSRPIGRANAEVP 186 ;
; LENGTH: 791
; TYPE: PRT
; ORGANISM: Artificial Sequence
; FEATURE: OTHER INFORMATION: sequence of plasminogen

Db 175 DGKISKTMMSGLEQWDSQSPHAGYIPLSKFPNKLKQYCRNPDRLRP----- 224 ;
; LENGTH: 791
; TYPE: PRT
; ORGANISM: mammalian

RESULT 8
US-10-304-287-1
; Sequence 1, Application US/10304287
; Publication No. US20030083234A1
; GENERAL INFORMATION:
; APPLICANT: Walisman, David M.
; TITLE OF INVENTION: Anti-angiogenesis methods, compositions and uses therefor
; FILE REFERENCE: ME02-001
; CURRENT APPLICATION NUMBER: US/10/304, 287
; CURRENT FILING DATE: 2002-11-25
; PRIORITY APPLICATION NUMBER: US 60/333, 866
; PRIORITY FILING DATE: 2001-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Word
; SEQ ID NO: 1
; LENGTH: 791
; TYPE: PRT
; ORGANISM: mammalian

US-10-304-287-1

Query Match 7.5%; Score 101; DB 14; Length 791;
Best Local Similarity 18.0%; Pred. No. 0; 24; Mismatches 90; Indels 110; Gaps 13;
Matches 53; Conservative 42; MisMatches 90; Indels 110; Gaps 13;

QY 5 LGVFAREVRSADSVRCLASACINAADFDFGFECESTWYYPDAECLNTEDR----LDRP 59 ;
; LENGTH: 791
; PRIORITY: 2002-01-01
; PRIORITY NUMBER: US 10/304, 287
; PRIORITY FILING DATE: 2002-11-28
; NUMBER OF SEQ ID NOS: 8
; SOFTWARE: Microsoft Word
; SEQ ID NO: 1
; LENGTH: 791
; TYPE: PRT
; ORGANISM: mammalian

RESULT 9
US-10-778-423-1
; Sequence 1, Application US/10778423
; Publication No. US2004132664A1
; GENERAL INFORMATION:
; APPLICANT: Abbott Laboratories
; APPLICANT: Henkin, Jack
; APPLICANT: Davidson, Donald J.
; TITLE OF INVENTION: ANTIANGIOGENIC POLYPEPTIDES AND METHODS
; FILE REFERENCE: 673B US. 02
; CURRENT APPLICATION NUMBER: US 10/778, 423
; CURRENT FILING DATE: 2004-02-13
; PRIORITY APPLICATION NUMBER: US/09/967, 386
; PRIORITY FILING DATE: 2001-09-28
; PRIORITY APPLICATION NUMBER: US 60/236, 550
; PRIORITY FILING DATE: 2000-09-29
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 791
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-778-423-1

Query Match 7.5%; Score 101; DB 16; Length 791;
Best Local Similarity 18.0%; Pred. No. 0.24; Mismatches 90; Indels 110; Gaps 13;
Matches 53; Conservative 42; MisMatches 90; Indels 110; Gaps 13;

QY 5 LGVFAREVSDSVRCLASACINAADFDFGFECESTWYYPDAECLNTEDR----LDRP 59 ;
; LENGTH: 791
; PRIORITY: 2002-01-01
; PRIORITY NUMBER: US 10/778423
; PRIORITY FILING DATE: 2004-02-13
; NUMBER OF SEQ ID NOS: 7
; SOFTWARE: FastSEQ for Windows Version 4.0
; SEQ ID NO: 1
; LENGTH: 791
; TYPE: PRT
; ORGANISM: Homo sapiens

US-10-778-423-1

RESULT 9
US-10-360-101-257
; Sequence 257, Application US/10360101
; Publication No. US2004009550A1
; GENERAL INFORMATION:
; APPLICANT: Moll, Gert N.
; APPLICANT: Deenhoups, Cornelis J.
; TITLE OF INVENTION: Export and modification of (poly)peptide in the lantibiotic way
; FILE REFERENCE: 2183-5673

RESULT 11
 US-10-733-646-1
 ; Sequence 1, Application US/10733646
 ; Publication No. US20040138127A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Abbott Laboratories
 ; ATTORNEY: David J. Davidson
 ; TITLE OF INVENTION: NOVEL ANTIANGIOGENIC PEPTIDES, POLYNUCLEOTIDES ENCODING SAME, AND METHODS FOR INHIBITING TITLE OF INVENTION: ANGIOGENESIS
 ; FILE REFERENCE: 5940 US P3
 ; CURRENT APPLICATION NUMBER: US/10/733, 646
 ; CURRENT FILING DATE: 2004-01-08
 ; PRIOR APPLICATION NUMBER: US/08/924, 287A
 ; PRIOR FILING DATE: 2004-01-08
 ; PRIOR APPLICATION NUMBER: US 08/851, 350
 ; PRIOR FILING DATE: 1997-05-05
 ; PRIOR APPLICATION NUMBER: US 08/832, 087
 ; PRIOR FILING DATE: 1997-04-03
 ; PRIOR APPLICATION NUMBER: US 08/643, 219
 ; PRIOR FILING DATE: 1996-05-03
 ; NUMBER OF SEQ ID NOS: 40
 ; SOFTWARE: FastSEQ for Windows Version 4.0
 ; SEQ ID NO 1
 ; LENGTH: 791
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-10-733-646-1

Query Match 7.5%; Score 101; DB 16; Length 791;
 Best Local Similarity 18.0%; Pred. No. 0.24; Mismatches 90; Indels 110; Gaps 13;
 Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

Qy 5 LVGFAREVVSADSVRCLSACLNAFDTGFPECESVMYYPDAECLNTEDR----LDRP 59
 Db 14 LFSVTEKK--VYISeCKTGYNGKNYRGTMSKTKNGITCQWST---SPH---- 114
 Qy 1420 RQLSDELDHSFEGLE----LSECELCITO---- 144
 Db 60 DLFVDEHEDTVIYDNNCAGCCECHWFDFNFKTSGLINDQFAIAQCYAPVTOVAVEG 119
 Qy 71 DVLVFEKK--VYISeCKTGYNGKNYRGTMSKTKNGITCQWST---SPH---- 114
 Db 115 RPRSPATHSEGLENVCRNPNDPQGWCYTDPKRYDYCILEBECMHCSGENY 174
 Qy 145 --RISVTANDFNCKS----FMSNLTRS-CVLSDRSPRPLGRNLAEVP 186
 Db 175 DGKISKTMSGLECQAWDSOPHANGYVSKFPNKLKKNYCRNDRELKP---- 224
 Qy 187 GWTYFESRGVPSFTRVQMLLVGFASFVMEVPSVTCMLDQCTSPPPETQNFVC 241
 Db 225 -W-----CFTDPN----KRWECDIP-----RCTTPPSSGPTYQC 256

RESULT 12
 US-10-735-577-1
 ; Sequence 1, Application US/10735577
 ; Publication No. US20040142897A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Walzman, David M.
 ; TITLE OF INVENTION: Compositions and Methods for Inhibiting Tumor Growth and Metastasis
 ; FILE REFERENCE: ME03-009
 ; CURRENT FILING DATE: 2003-12-12
 ; PRIOR APPLICATION NUMBER: US 60/433, 140
 ; PRIOR FILING DATE: 2002-12-13
 ; NUMBER OF SEQ ID NOS: 160
 ; SOFTWARE: Microsoft Word
 ; SEQ ID NO 1
 ; LENGTH: 791
 ; TYPE: PRT
 ; ORGANISM: mammalian
 ; US-10-735-577-1

Query Match 7.5%; Score 101; DB 16; Length 791;
 Best Local Similarity 18.0%; Pred. No. 0.24; Mismatches 90; Indels 110; Gaps 13;
 Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

Qy 5 LVGFAREVVSADSVRCLSACLNAFDTGFPECESVMYYPDAECLNTEDR----LDRP 59
 Db 71 DVLVFEKK--VYISeCKTGYNGKNYRGTMSKTKNGITCQWST---SPH---- 114
 Qy 1420 RQLSDELDHSFEGLE----LSECELCITO---- 144
 Db 60 DLFVDEHEDTVIYDNNCAGCCECHWFDFNFKTSGLINDQFAIAQCYAPVTOVAVEG 119
 Qy 71 DVLVFEKK--VYISeCKTGYNGKNYRGTMSKTKNGITCQWST---SPH---- 114
 Db 115 RPRSPATHSEGLENVCRNPNDPQGWCYTDPKRYDYCILEBECMHCSGENY 174
 Qy 145 --RISVTANDFNCKS----FMSNLTRS-CVLSDRSPRPLGRNLAEVP 186
 Db 175 DGKISKTMSGLECQAWDSOPHANGYVSKFPNKLKKNYCRNDRELKP---- 224
 Qy 187 GWTYFESRGVPSFTRVQMLLVGFASFVMEVPSVTCMLDQCTSPPPETQNFVC 241
 Db 225 -W-----CFTDPN----KRWECDIP-----RCTTPPSSGPTYQC 256

RESULT 13
 US-09-946-893-2
 ; Sequence 2, Application US/09946893
 ; Patent No. US20020072494A1
 ; GENERAL INFORMATION:
 ; APPLICANT: Cao, Yihai
 ; TITLE OF INVENTION: Materials and methods relating to endothelial cell growth inhibitor
 ; FILE REFERENCE: Mewurn
 ; CURRENT APPLICATION NUMBER: US/09/946, 893
 ; CURRENT FILING DATE: 2001-09-05
 ; PRIOR APPLICATION NUMBER: US 60/230, 893
 ; PRIOR FILING DATE: 2000-09-05
 ; NUMBER OF SEQ ID NOS: 11
 ; SOFTWARE: PatentIn Ver. 2.1
 ; SEQ ID NO 2
 ; LENGTH: 810
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; US-09-946-893-2

Query Match 7.5%; Score 101; DB 9; Length 810;
 Best Local Similarity 18.0%; Pred. No. 0.25; Mismatches 90; Indels 110; Gaps 13;
 Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

Qy 5 LVGFAREVVSADSVRCLSACLNAFDTGFPECESVMYYPDAECLNTEDR----LDRP 59
 Db 33 LFSVTEKK--VYISeCKTGYNGKNYRGTMSKTKNGITCQWST---SPH---- 114
 Qy 60 DLFVDEHEDTVIYDNNCAGCCECHWFDFNFKTSGLINDQFAIAQCYAPVTOVAVEG 119

RESULT 14
 US-10-193-656-2
 ; Sequence 2, Application US/10193656
 ; Publication No. US2003009673A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NY, Tor
 ; APPLICANT: HELIESTROM, Sten
 ; APPLICANT: ERIKSSON, Per-Olof
 ; TITLE OF INVENTION: METHOD OF WOUND HEALING
 ; FILE REFERENCE: 3810/1J759-US1
 ; CURRENT APPLICATION NUMBER: US/10/237,144
 ; CURRENT FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/317,643
 ; PRIOR FILING DATE: 2001-09-06
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO: 1
 ; LENGTH: 810
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: GenBank / 625234
 ; DATABASE ENTRY DATE: 2000-09-15
 ; RELEVANT RESIDUES: (1)..(810)
 ; US-10-237-144-1

Query Match 7.5%; Score 101; DB 14; Length 810;
 Best Local Similarity 18 0%; Pred. No. 0.25; Mismatches 90; Indels 110; Gaps 13;
 Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

Qy 5 LVGFAREVVSASVHRCILSACHNAFDTPGFECESVMMYPVDPEDCILNTEDR----LDRP 59
 Db 33 LFSVTKQLGAGSIECKACBEEDE--FTCRAFOYHSKQOCVIMAENRKSSTIIRMR 89
 Qy 60 DIFVDEHEDTWYILDNNCAGCCEWHIDNFKPSKTSGLINDQQFAIAACQYAPVYQAVEG 119
 Db 33 LFSVTKQLGAGSIECKACBEEDE--FTCRAFOYHSKQOCVIMAENRKSSTIIRMR 89
 Qy 60 DLFVDBHEDTWYILDNNCAGCCEWHIDNFKPSKTSGLINDQQFAIAACQYAPVYQAVEG 119
 Db 90 DVLFLEKK--VYLSECKTGNCAGKNYRGTMSKTKNGITCQWSST----SPH----- 133
 Qy 120 ROLSDELDHSEFGL-----LSBCEELCTQ----- 144
 Db 134 RFRFSPATHPSQGLEEYCRNFDNDPQGPWCITDPEKRYYQDILCECERCMHCSGENY 193
 Qy 145 --RLSVTANDFNCKS-----FMSNLTRS-CVLSRSRPLGRANLAEV 186
 Db 194 DGKISKTMMSGLEQAWDSOSPHAHGYIPSKEPNKNLKKYCNCPDRBLRP----- 243
 Qy 187 GWTYFESRGVPSFTRVQMLLVGFASFTVNMENVPSVTCMLDQCTSPPETQNFVC 241
 Db 244 -W-----CFTTDPN-----KRWELCDIP-----RCTTPPSSGPTYQC 275

Publication No. US20030147879A1
 ; GENERAL INFORMATION:
 ; APPLICANT: NY, Tor
 ; APPLICANT: LI, Jian
 ; APPLICANT: HELIESTROM, Sten
 ; APPLICANT: ERIKSSON, Per-Olof
 ; TITLE OF INVENTION: METHOD OF WOUND HEALING
 ; FILE REFERENCE: 3810/1J759-US1
 ; CURRENT APPLICATION NUMBER: US/10/237,144
 ; CURRENT FILING DATE: 2002-09-05
 ; PRIOR APPLICATION NUMBER: US 60/317,643
 ; PRIOR FILING DATE: 2001-09-06
 ; NUMBER OF SEQ ID NOS: 5
 ; SOFTWARE: Patentin version 3.1
 ; SEQ ID NO: 1
 ; LENGTH: 810
 ; TYPE: PRT
 ; ORGANISM: Homo sapiens
 ; PUBLICATION INFORMATION:
 ; DATABASE ACCESSION NUMBER: GenBank / 625234
 ; DATABASE ENTRY DATE: 2000-09-15
 ; RELEVANT RESIDUES: (1)..(810)
 ; US-10-193-656-2

Query Match 7.5%; Score 101; DB 14; Length 810;
 Best Local Similarity 18 0%; Pred. No. 0.25; Mismatches 90; Indels 110; Gaps 13;
 Matches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

Qy 5 LVGFAREVVSASVHRCILSACHNAFDTPGFECESVMMYPVDPEDCILNTEDR----LDRP 59
 Db 33 LFSVTKQLGAGSIECKACBEEDE--FTCRAFOYHSKQOCVIMAENRKSSTIIRMR 89
 Qy 60 DLFVDBHEDTWYILDNNCAGCCEWHIDNFKPSKTSGLINDQQFAIAACQYAPVYQAVEG 119
 Db 90 DVLFLEKK--VYLSECKTGNCAGKNYRGTMSKTKNGITCQWSST----SPH----- 133
 Qy 120 ROLSDELDHSEFGL-----LSBCEELCTQ----- 144
 Db 134 RFRFSPATHPSQGLEEYCRNFDNDPQGPWCITDPEKRYYQDILCECERCMHCSGENY 193
 Qy 145 --RLSVTANDFNCKS-----FMSNLTRS-CVLSRSRPLGRANLAEV 186
 Db 194 DGKISKTMMSGLEQAWDSOSPHAHGYIPSKEPNKNLKKYCNCPDRBLRP----- 243
 Qy 187 GWTYFESRGVPSFTRVQMLLVGFASFTVNMENVPSVTCMLDQCTSPPETQNFVC 241
 Db 244 -W-----CFTTDPN-----KRWELCDIP-----RCTTPPSSGPTYQC 275

Search completed: March 31, 2005, 02:10:10
 Job time : 142 SECs

RESULT 15
 US-10-237-144-1
 ; Sequence 1, Application US/10237144

GenCore version 5.1.6
Copyright (c) 1993 - 2005 Compugen Ltd.

OM protein - protein search, using sw model

Run on: March 31, 2005, 01:56:55 ; Search time 43 Seconds

Perfect score: 1354 ; US-10-771-708-11

Sequence: 1 EOKILVGFAREVVSADSVHR PPPETGQNFCVCKSVMMYYNE 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched:

283416 seqs, 96216763 residues

Total number of hits satisfying chosen parameters: 283416

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%

Listing first 45 summaries

Database : PIR_79;*

1: pir1;*
2: pir2;*
3: pir3;*
4: pir4;*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

RESULT 1

C87789 protein C34G6_6 [imported] - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Jul-2004
C;Accession: C87789
R;Anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome Sequence of the nematode *C. elegans*: a platform for investigating biology
A;Reference number: A75000; MUID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gcb/C_elegans/ and www.sanger.ac.uk/Projects/C_elegans/ and www.jcvi.org/celegans/ and www.ncbi.nlm.nih.gov/Genomes/

A;Accession: C87789
A;Status: preliminary
A;Molecule type: DNA
A;Residues: j-1011 <STO>
A;Cross-references: UNIPROT:001494; GB:chr_I; PIDN:AA852479.1; PID:gi1943841; GSPDB:GN0001
C;Genetics:
A;Gene: C34G6.6
A;Map position: 1

Query Match 67.4%; Score 912.5; DB 2; Length 1011; Best Local Similarity 66.2%; Pred. No. 12e-75; Matches 172; Conservative 33; Mismatches 36; Indels 19; Gaps 5;

Qy 1 EOKILVGFAREVVSADSVHR.....
Db 114 EOKILVGFAREVVSADSVHR.....
Qy 61 LFVDEBHDFTVYLDNCAGCECHWFDNFKTSGILNDQOFATA-AQCYVLPYVTOVAVEG 119
Db 174 LFVDEBHDFTVYLDNCAGCPL- VFKNY-----NYQKTFSKSQCYPYIOTQIAYEG 225

Qy 120 RQLSDELDNSFEGELSEFELCTQRLSTANDNCNSMYSNLTSCVLSDESRPLR 179
Db 226 KOLKNEBLRIT-NYLDLSDCQALCQKLTSSNDFKNSHNNKTRCTLADERSKPLR 284

Qy 180 ANLAEVPGTYFES-----RGVPSTTRVQMLLVCFASFEMENVSVTMQLDQCT 230

Db 285 ADLATEGVYFEKCFAPAQNPTCRNVPSPFKRVPOMILVCFAAFMENVSVTMQLDQCTN 344

Db 345 PPPETGQNFCVCKSVMMYYNE 364

RESULT 2

T21967 hypothetical protein F38E11.4 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T21967

protein with DnaJ

R;Matthews, P.
submitted to the EMBL Data Library, January 1996
A;Reference number: Z19495
A;Accession: T21967
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-751 <WIL>
A;Cross-references: UNIPROT:Q20167; EMBL:Z68342; PIDN:CAA92773.1; GSPDB:GN00022; CESP:F3
A;Experimental source: clone F38E11
C;Genetics:
A;Gene: CESP:F38E11.4
A;Map position: 4
A;Introns: 23/1; 68/3; 115/1; 210/1; 284/1; 307/1; 359/3; 539/3; 622/2; 660/1; 695/2

Query Match 19.4%; Score 262; DB 2; Length 751;
Best Local Similarity 27.4%; Pred. No. 5 7e-16;
Matches 73; Conservative 37; Mismatches 98; Indels 58; Gaps 8;

Qy 2 OKILVGFAREKVSADSVRCSACINAFDFERFECESVNYVYDASCILNTEDRDRPDL 61
Db 131 QSLIGHAMKVLIVDGLSDCLSCALQSRSYFLCKSAIYVYETGECIMRNDRKFTYPL 190

Qy 62 FVDEDEHEDVTI-YLDNNCAGCEC----HWHHDNFKTSGLINDQQFIAACQYAPVQY 114
Db 191 FKNHILDLTFLVDFENNADVSCKPEELHW----- 220

Qy 115 VAVEGROLSDLDHSFEGLELSCEELCTQRISVANDFNCKSFMSNLTRSCVSDERS 174
Db 221 VRTTEYLIDESKVIVESSDAGECNQLC-QNNKIGEENPCKAFAYNSKCECHLAESS 279

Qy 175 ---RPLGRANALAEVPGWYFESRGVP-----SPTRVQMLLVGFASFMENVPST 222
Db 280 YVGHKGDKRKNLAPLNSGBYFHKCLPNTNQCLIEASPELVAARMMT--SAYKTTISALQH 337

Qy 223 MLDQCTSPPPPTGQNIVCKSYMMY 248
Db 338 ECLSQCMNDGAR-----CSSAIVFY 357

RESULT 3

T22486 hypothetical protein F52B11.3 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
C;Accession: T22486
R;Matthews, L.
A;Reference number: 219569
A;Accession: T22486
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Residues: 1-441 <WIL>
A;Cross-references: UNIPROT:Q9XUE5; EMBL:Z82268; PIDN:CAB05199.1; GSPDB:GN00022; CESP:F52B11.1
A;Experimental source: clone F52B11
C;Genetics:
A;Gene: CESP:F52B11.3
A;Map position: 4
A;Introns: 48/1; 298/1; 341/3; 690/2

Query Match 12.4%; Score 168; DB 2; Length 741;
Best Local Similarity 22.5%; Pred. No. 2.5e-07; Mismatches 100; Indels 124; Gaps 15;
Matches 76; Conservative 38; Mismatches 100; Indels 124; Gaps 15;

Qy 5 LVGFARREVSADSVRHCLSACLNAFDGFBCEESVNYVYDAAECLNTEDRDRPLFVD 64
Db 137 LEGFVFKSVTENREHCLSACIKEE--FVCKSIVFHYTSLCSELSVEDKRSKP---- 188

Qy 65 EH--EDTVIYIDNNGAG-----C--EC 82
Db 189 THVRMSEKIDYIDNCLSLRQNRCCGSGGNNLVFKVKTNEIYDHTQSVAQESYCLQK 248

Qy 83 HWHEDDFPKTSCILN-----DQQ-----FAIAQCYAPVQY 114

RESULT 4

G89459 protein C52B11.1 [imported] - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 10-May-2001 #sequence_revision 10-May-2001 #text_change 09-Nov-2001
C;Accession: G89459
R;anonymous, The C. elegans Sequencing Consortium.
Science 282, 2012-2018, 1998
A;Title: Genome sequence of the nematode *C. elegans*: a platform for investigating biology
A;Residues: A75000; PMID:99069613; PMID:9851916
A;Note: see websites genome.wustl.edu/gsc/c_elegans/ and www.sanger.ac.uk/Projects/C_elegans
A;Accession: G89459
A;Status: preliminary
A;Molecule type: DNA
A;Residues: 1-282 <STO>
A;Cross-references: GB:chr_X; PIDN:AAA82467.1; PID:g1086885; GSPDB:GN00028; CESP:C52B11.1
A;Genetics:
A;Map position: X

Query Match 11.8%; Score 160; DB 2; Length 282;
Best Local Similarity 28.9%; Pred. No. 4.1e-07; Mismatches 71; Indels 18; Gaps 4;
Matches 43; Conservative 17; Mismatches 71; Indels 18; Gaps 4;

Qy 112 TQYVAVEGROLSDLDHSFEGLELSCEELCTQRISVANDFNCKSFMSNLTRSCVLSD 171
Db 31 THFVTDNALSQADPIVVKATSEBECCLACTQRISVANDFNCKSFMSNLTRSCVLSD 171

Qy 172 ERSRPLGRANALAEVPGWTFE---SRGP-----SPTRVQMLLVGFASFMENVPST 221
Db 91 EKSAPVGSQIENSVGKRYFKEKILSHNPQQCQTQFIVDQSVLGYA-VNMTLDSI 149

Qy 222 TMCLDQCTSPPPPTGQNIVCKSYMMY 250
Db 150 ESCAAQCV-----QEADCKSAMVYED 171

RESULT 5

T32444 hypothetical protein H42K12.3 - *Caenorhabditis elegans*
C;Species: *Caenorhabditis elegans*
C;Date: 29-Oct-1999 #sequence_revision 29-Oct-1999 #text_change 09-Jul-2004
C;Accession: T32444; T15821
R;Maggi, L.; Harper, M.
A;Reference number: 221169
A;Accession: T32444
A;Status: preliminary; translated from GB/EMBL/DDBJ
A;Molecule type: DNA
A;Residues: 1-522 <MAG>
A;Cross-references: UNIPROT:O17347; EMBL:AE026207; PIDN:AA871266.1; GSPDB:GN00028; CESP:F52B11
A;Experimental source: strain Bristol N2; clone H42K12
R;Martin, J.
A;Submitted to the EMBL Data Library, November 1995
A;Description: The sequence of *C. elegans* cosmid C52B11.
A;Reference number: Z18411

A;Accession: T15821
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-351 <WIL>
 A;Cross-references: UNIPROT:Q21782; EMBL:Z67756; PIDN:CAA91764_1; GSPDB:GN00028; CESP:R07A4-4
 A;Experimental source: strain Bristol N2
 C;Genetics:
 C;Gene: CESP:H42K12.3; CESP:C52B11.1
 A;Map position: X
 A;Introns: 24/1; 65/3; 117/1; 163/3; 208/1; 281/1; 381/3; 430/1; 481/3
 Query Match 11.8%; Score 160; DB 2; Length 522;
 Best Local Similarity 28.9%; Pred. No. 8.7e-07; DB 2; Length 522;
 Matches 43; Conservative 17; Mismatches 71; Indels 18; Gaps 4;
 Qy 112 TQYVAVEGRLSDELDHSFEGGLELSECELCQTQRLSUTANDDFNCFSFPMYSNLRSCLSD 171
 Db 31 THFVVDNDSLQSAQPIVVKATSERBECLEACTKNDKFRPVCFTVHASSCTIK 90
 Qy 172 ERSRPLGRANLALAEVPGWTFFE---SRGVVP-----SFRVPPQMLVNGASFWMENVPSV 221
 Db 91 EKSAAPVGSAQIENSVGKRYFEKICLUSHNIPQCAOTQIFRUDQSVLNGTA-VNNLTDSDI 149
 Qy 222 TMCUQOCTSPPETGQNFVCKSVMYTYNE 250
 Db 150 ECAQACV-----QEADCKSAMFYED 171

RESULT 6
 T29557 hypothetical protein C16D9.1 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T29557
 C;Gattting: S.; Le, T.T.
 Submitted to the EMBL Data Library, July 1996
 A;Description: The sequence of *C. elegans* cosmid C16D9.
 A;Reference number: 220640
 A;Accession: T29557
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-342 <GAP>
 A;Cross-references: UNIPROT:Q22902; EMBL:U64058; PIDN:AAB19288_1; GSPDB:GN00023; CESP:C1
 A;Experimental source: strain Bristol N2; clone C16D9
 A;Gene: CESP:C16D9.1
 A;Map position: 5
 A;Introns: 59/2; 316/3
 Query Match 11.3%; Score 153.5; DB 2; Length 342;
 Best Local Similarity 38.2%; Pred. No. 2.1e-06; DB 2; Length 342;
 Matches 29; Conservative 16; Mismatches 26; Indels 3; Gaps 2;
 Qy 3 KILVGFAREVV-SADSVHRLCLACINAFDFGFECESSVMYPPVDPRECLNTEDRDRPDL 61
 Db 121 KVLIGIVDQLVRDVATVNDQACQCSNSQTKYDICKSAMYKEKRECILASQSKADIPDL 180
 Qy 62 FVDEHDTVYLDNNG 77
 Db 181 FID-DDKSILYIENSC 194

RESULT 7
 T23990 hypothetical protein R07M4.4 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T23990
 C;Cottage, A.
 submitted to the EMBL Data Library, November 1995
 A;Reference number: Z19827
 A;Accession: T23990
 A;Status: preliminary; translated from GB/EMBL/DBJ

RESULT 8
 T28804 hypothetical protein H03E18.1 - *Caenorhabditis elegans*
 C;Species: *Caenorhabditis elegans*
 C;Date: 15-Oct-1999 #sequence_revision 15-Oct-1999 #text_change 09-Jul-2004
 C;Accession: T28804
 R;Bentley, D.
 submitted to the EMBL Data Library, August 1996
 A;Description: The sequence of *C. elegans* cosmid H03E18.
 A;Reference number: 220900
 A;Accession: T28804
 A;Status: preliminary; translated from GB/EMBL/DBJ
 A;Molecule type: DNA
 A;Residues: 1-117 <BEN>
 A;Cross-references: UNIPROT:Q94248; EMBL:UG7947; PIDN:AAB07557_1; GSPDB:GN00028; CESP:HO:
 A;Experimental source: strain Bristol N2; clone H03E18
 C;Genetics:
 C;Gene: CESP:H03E18.1
 A;Map position: X
 A;Introns: 112/3; 217/1; 282/2; 304/1; 424/1; 461/2; 579/3; 615/2; 831/1; 999/2; 1088/1
 Query Match 9.2%; Score 124.5; DB 2; Length 1127;
 Best Local Similarity 22.3%; Pred. No. 0.0041; DB 2; Length 1127;
 Matches 44; Conservative 37; Mismatches 75; Indels 41; Gaps 9;
 Qy 1 EOKTILGFAREVV-SADSVHRLCLACINAFDFGFECESSVMYPPVDPRECLNTEDRDR 58
 Db 433 DDHLMVSVAGGLEDMSIETRCQCMANCNSRRFEPQCSATVYHAEKICLNLDRNTR 492
 Qy 59 PDLFVDEHDTVYLDNNG-----AGCECHWHD-----NEFTSGIL 95
 Db 493 SKLFFKQFDVNVVYIGLACEVDEUTVSKGSLSLATEGRKVEATGEPKETSKKNGIK 552
 Qy 96 NDQOFAIAQACYAPVVTQVAVEGRLSDELDHSFEGGLELSECELCQRLSUTANDDFNC 155
 Db 553 SD-----DCYVE-LNDTV-LEGTAIAVE-----TAVTPEECKCAGHKLGYEE-C 596
 Qy 155 KSFMYSNLRSCLSD 172
 Db 597 ASFLVYDDBKCLINKQ 613

RESULT 9
 PLG
 plasmin (EC 3.4.21.7) precursor - pig (fragment)
 N;Alternate names: plaminogen
 N;Contains: miniplasminogen

RESULT 10

Qy	132 GELSECERLCTQRLSIVTANDPNCKSPMFMSNLTRSCVLSIDRS	174
Db	408 VENQDCWSLCVN-----SKVCELEISFTTSNQCLLTS	444
RESULT 14		
PLRU	Plasmin (EC 3.4.21.7) precursor [validated] - human	
N;Alternate name:	plasminogen precursor [mismomer]	
N;Contains:	angiotensin; microplasmin; plasminogen	
N;Species:	Homo sapiens (man)	
C;Date:	24-Apr-1984 #sequence revision 02-Dec-1994 #text-change 09-Jul-2004	
C;Accession:	A55229; 15242; A26646; 162738; 184609; S03735; A00929; A04627; A04625; A04	
R;Petersen, T.E.; Martzen, M.R.; Ichinose, A.; Davie, E.W.		
R;Biol. Chem. 265, 6104-6111, 1990		
A;Title:	Characterization of the gene for human plasminogen, a key proenzyme in the fibrinolytic system	
A;Reference number:	A35229; MUID:9020879; PMID:218848	
A;Accession:	A35229	
A;Molecule type:	DNA	
A;Residues:	1-810 <PRT>	
A;Cross-references:	UNIPROT:P00747; UNIPROT:Q9UBQ9; UNIPROT:Q9UM12; GB:J05286; GB:M34276	
A;Experimental source:	leukocyte; lung fibroblast	
R;Malagrétti, N.; Bruno, I.; Pontoglio, M.; Candiani, G.; Mezoni, G.; Ottolenghi, S.; Tamburini, B.; Biochem. Biophys. Res. Commun. 173, 1013-1018, 1990		
A;Title:	Definition of the transcription initiation site of human plasminogen gene in leukocytes	
A;Reference number:	I5242; MUID:91097523; PMID:2268308	
A;Accession:	I5242	
A;Statusus:	translated from GB/EMBL/DBJ	
A;Molecule type:	DNA	
A;Residues:	1-16 <MAIL>	
A;Cross-references:	GB:MG2890; NID:9190032; PIDN:AAA36454.1; PID:95553613	
R;Forssgren, M.; Raden, B.; Israelsson, M.; Larsson, K.; Heden, L.O.		
REBS Lett. 213, 254-260, 1987		
A;Title:	Molecular cloning and characterization of a full-length cDNA clone for human plasminogen	
A;Reference number:	A26646; MUID:87162490; PMID:300813	
A;Accession:	A26646	
A;Molecule type:	mRNA	
A;Residues:	1-471, 'D', 473-810 <FOR>	
A;Cross-references:	GB:X05199; NID:935530; PIDN:CAA28831.1; PID:935531	
A;Experimental source:	liver	
R;Malinowski, D.P.; Sadler, J.E.; Davie, E.W.		
Biochemistry 23, 4243-4250, 1984		
A;Title:	Characterization of a complementary deoxyribonucleic acid coding for human and bovine plasminogen	
A;Reference number:	I45961; MUID:85023311; PMID:6148961	
A;Accession:	I45961	
A;Statusus:	translated from GB/EMBL/DBJ	
A;Molecule type:	DNA	
A;Residues:	367-419 <MAIL>	
A;Cross-references:	GB:K02291; NID:9190110; PIDN:AAA60124.1; PID:9387031	
A;Accession:	I84609	
A;Statusus:	translated from GB/EMBL/DBJ	
A;Molecule type:	mRNA	
A;Residues:	292-471, 'D', 473-810 <MAIL>	
A;Cross-references:	GB:K02292; NID:9190112; PIDN:AAA60124.1; PID:9387031	
A;Accession:	I84609	
A;Statusus:	translated from GB/EMBL/DBJ	
A;Molecule type:	DNA	
A;Residues:	292-471, 'D', 473-810 <MAIL>	
A;Cross-references:	GB:K02291; NID:9190110; PIDN:AAA60124.1; PID:9387031	
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A;Molecule type:	protein	
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A;Cross-references:	GB:K02291; NID:9190110; PIDN:AAA60124.1; PID:9387031	
A;Accession:	I84609	
A;Statusus:	submitted to the Atlas, July 1977	
A;Title:	Comparison of the primary structure of the N-terminal CNBr fragments of human, bovine and porcine plasminogen	
A;Reference number:	S03735; MUID:81212097; PMID:7238497	
A;Accession:	S03735	
A;Molecule type:	protein	
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A;Cross-references:	GB:K02291; NID:9190110; PIDN:AAA60124.1; PID:9387031	
A;Accession:	I84609	
A;Statusus:	submitted to the Atlas, July 1977	
A;Title:	Comparison of the primary structure of the N-terminal CNBr fragments of human, bovine and porcine plasminogen	
A;Reference number:	S03735; MUID:81212097; PMID:7238497	
A;Accession:	A00929	
A;Molecule type:	protein	
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A;Residues:	20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>	
A;Cross-references:	GB:K02291; NID:9190110; PIDN:AAA60124.1; PID:9387031	
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A;Residues:	20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>	
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A;Molecule type:	protein	
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A;Accession:	A00929	
A;Molecule type:	protein	
A;Residues:	20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>	
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A;Accession:	A00929	
A;Molecule type:	protein	
A;Residues:	20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>	
A;Cross-references:	GB:K02291; NID:9190110; PIDN:AAA60124.1; PID:9387031	
A;Accession:	A00929	
A;Molecule type:	protein	
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A;Accession:	A00929	
A;Molecule type:	protein	
A;Residues:	20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>	
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A;Molecule type:	protein	
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A;Residues:	20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>	
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A;Molecule type:	protein	
A;Residues:	20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>	
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A;Molecule type:	protein	
A;Residues:	20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>	
A;Cross-references:	GB:K02291; NID:9190110; PIDN:AAA60124.1; PID:9387031	
A;Accession:	A00929	
A;Molecule type:	protein	
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A;Molecule type:	protein	
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A;Molecule type:	protein	
A;Residues:	20-71, 'E', 73-85, 87-106, 'D', 108-360, 'E', 362-810 <SOT>	
A;Cross-references:</		

A;Title: Crystal and molecular structure of human plasminogen kringle 4 refined at 1.9 A
 A;Reference number: A58019; MUID:92031502; PMID:1657148
 A;Contents: annotation
 R;NU, T.P.; Padmanabhan, K.; Tulinsky, A.; Mulichak, A.M.
 Biochemistry 30, 10589-10594, 1991
 A;Title: The refined structure of the epsilon-aminocaproic acid complex of human plasmin
 A;Reference number: A58018; MUID:92031503; PMID:1657149
 A;Contents: annotation
 R;de Vos, A.M.; Uitsch, M.H.; Kelley, R.F.; Padmanabhan, K.; Tulinsky, A.; Westbrook, M.
 Biochemistry 31, 270-279, 1992
 A;Title: Crystal structure of the kringle 2 domain of tissue plasminogen activator at 2.
 A;Reference number: A59483; MUID:9211803; PMID:1310033
 A;Contents: annotation; X-ray crystallography, 2.4 angstroms
 R;Stec, B.; Teeter, M.M.; Whitlow, M.; Yamano, A.
 submitted to the Brookhaven Protein Data Bank, June 1995
 A;Reference number: A65980; PDB:1KRN
 A;Contents: annotation; X-ray crystallography, 1.67 angstroms, residues 376-454
 submitted to the Brookhaven Protein Data Bank, August 1996
 A;Reference number: A65803; PDB:1MPJ
 A;Contents: annotation; conformation by (1)H-NMR, residues 103-181
 R;Rejante, M.; Llinas, M.
 submitted to the Brookhaven Protein Data Bank, August 1996
 A;Reference number: A65804; PDB:1HPK
 A;Contents: annotation; conformation by (1)H-NMR, residues 103-181
 R;Rejante, M.R.; Llinas, M.
 Eur. J. Biochem. 221, 927-937, 1994
 A;Title: (1)H-NMR assignments and secondary structure of human plasminogen kringle 1.
 A;Reference number: S41645; MUID:94231157; PMID:8181475
 A;Contents: annotation; conformation by (1)H-NMR, residues 96-184
 R;Rejante, M.R.; Llinas, M.
 Eur. J. Biochem. 221, 939-949, 1994
 A;Title: Structure of the epsilon-aminohexanoic acid complex of human plasminogen
 A;Reference number: A58817; MUID:94231158; PMID:8181476
 A;Contents: annotation; conformation by (1)H-NMR, residues 96-184
 C;Comment: Plasminogen is synthesized by the kidney and is present in plasma and many other
 C;Comment: Plasminogen is converted to plasmin by plasminogen activators (see PIR:UKHU and
 PIR:FGUGB).
 C;Comment: Plasmin is inactivated by alpha-2-antiplasmin (see PIR:IFHUA2) immediately after
 C;Comment: Plasmin is formed by autolytic cleavage of plasmin under artificial conditions
 C;Comment: Microplasmin is formed by autolytic cleavage of plasmin to produce angiotatin. This
 C;Comment: Stromelysin 1 (see PIR:KCHS1) acts on plasminogen to produce angiotatin. This
 C;Genetics:
 A;Gene: GDB:PLG
 A;Cross-references: GDB:119498; OMIM:173350
 A;Map position: 6026-6027
 A;Intron: 17/1; 62/2; 98/1; 136/2; 183/1; 223/2; 263/1; 317/2; 366/1; 419/2; 480/1; 529
 C;Function:
 A;Description: dissolves the fibrin of blood clots; acts as a proteolytic factor in a variety of
 A;Pathway: fibrinolysis
 C;Superfamily: plasmin; kringle homology; plasminogen-related protein precursor homology
 C;Keywords: angiogenesis; inhibitor; blood; fibrinolysis; plasminogen; glycoprotein; hydrolase
 F;1-96/Domain: plasminogen-related protein precursor homology <PLPHs>
 F;1-19/Domain: signal sequence #status experimental <PRO>
 F;20-96/Domain: activation peptide #status experimental <PRO>
 F;1-9-466/Domain: angiostatin #status experimental <AST>
 F;97-580/Domain: plasmin chain A #status experimental <CHA>
 F;103-181/Domain: kringle homology <KR1>
 F;185-262/Domain: kringle homology <KR2>
 F;275-352/Domain: kringle homology <KR3>
 F;377-454/Domain: kringle homology <KR4>
 F;481-560/Domain: kringle homology <KR5>
 F;550-580, 581-810/Domain: microplasmin #status experimental <MMT>
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 Best Local Similarity 18.0%; Pred. No. 0.4; Mismatches 53; Conservative 42; Mismatches 90; Indels 110; Gaps 13;

Db 33 LFSVTKKQGAGSIEECKCEEDEE--FTCRAFOVHSKEQCGVIMANRKESIIIRR 89
 QY 60 DLVFDHEDEHTVILDNNGCAGCCEWHFDNPKISGLNQOFAIAQCYTPVQWAVE 119
 Db 90 DVVFEKK--VVLSECKINGKNGYRGMSKTRNGTICKWSS---SPH----- 133
 Db 120 RQLSDELDLISFPEGLE-----LSECETLCTQ----- 144
 QY 134 RPRSPATPHPSEGLENVCRNPNDPQGFWCYTDPEKRYDQDILECBBECMHCSGENY 193
 QY 145 --RLSVTADNFNEK-----FMSNLTS-CVLSDESSRPLGRNLAEP 186
 Db 194 DGKISKTMWSGLECOAWDSQSPHAGYTPSKFPNKNLKGKNCRNPDRELKP----- 243
 QY 187 GWTYFESRGVPSFTRVQMLVGFASFVNIVSVMCLQCTSPPPETGQNFC 241
 Db 244 -W-----CFTRDP-----KRMEDCIP-----RCTTPPSSGPTYQC 275
 Result 15
 T2288 hypothetical protein T26C5.2 - Caenorhabditis elegans
 C;Species: Caenorhabditis elegans
 C;Accession: T2288
 R;Thomas, K.
 submitted to the EMBL Data Library, August 1995
 A;Reference number: 220011
 A;Accession: T25288
 A;Status: preliminary; translated from GB/EMBL/DDJB
 A;Molecule type: DNA
 A;Residues: 1-554 <WIL>
 A;Cross-references: UNIPROT:Q22815; EMBL:250859; PIDN:CAA90727.1; GSPDB:GN00020; CESP:T26C5
 A;Experimental source: clone T26C5
 C;Genetics:
 A;Gene: CESP:T26C5.2
 A;Map position: 2
 A;Intron: 20/1; 59/3; 103/1; 266/1; 333/1; 376/3; 542/2
 C;Superfamily: Caenorhabditis elegans hypothetical protein T26C5.2
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 Best Local Similarity 28.8%; Pred. No. 0.35; Mismatches 33; Indels 3; Gaps 1;
 Matches 19; Conservative 11; Mismatches 33; Indels 3; Gaps 1;
 QY 16 DSVRCLSLACINAADFGEFCECSMMYVDAECLINTPDRDLPFDHEDEHTVILDN 75
 Db 455 DGMOLCIECVLSIK--FTCRSTENPTGQRLMTDSMSPDSEFDEKALYEN 512
 QY 76 NCAGCE 81
 Db 513 GCTNAE 518
 Search completed: March 31, 2005, 02:06:55
 Job time : 45 secs

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On protein - protein search, using sw model

Run on: March 31, 2005, 01:56:09 ; Search time 177 Seconds

Post-processing: Maximum Match 0% (without alignments) 723.276 Million cell updates/sec

Title: US-10-771-708-11

Perfect score: 1354

Sequence: 1 BQKILVGFAREVVSADSVHR..... PPPETGQNFVCKSVMYYNE 250

Scoring table: BLOSUM62

Gapop 10.0 , Gapext 0.5

Searched: 1612378 Seqs, 512079187 residues

Total number of hits satisfying chosen parameters: 1612378

Minimum DB seq length: 0

Maximum DB seq length: 200000000

Post-processing: Maximum Match 0% (without alignments)

Listing first 45 summaries

Database : UniProt 03:*

1: uniprot_sprot:*

2: uniprot_trembl:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	912.5	67.4	1065	001494
2	912.5	67.4	1069	0873B7
3	19.4	2	202167	caenorhabdi
4	168	12.4	741	09XUE5
5	160	11.8	522	017347
6	157	11.6	1494	07PTE3
7	153.5	11.3	398	022902
8	138	10.2	1549	08MK23
9	138	10.2	1549	09BMD4
10	138	10.2	1557	09BMD5
11	138	10.2	1557	09V5X3
12	126	9.3	351	021782
13	125	9.2	774	09V9X1
14	124.5	9.2	1127	094248
15	121	8.9	744	09VAG2
16	120.5	8.9	432	07PLU3
17	120.5	8.9	601	09W5Z0
18	120.5	8.9	715	2 08MS37
19	119.5	8.8	633	07QBU4
20	118.5	8.8	695	2 07QD96
21	116	8.6	790	1 PLMN_PIG
22	115	8.5	805	2 08IG52
23	113	8.3	833	2 09V9X0
24	108	8.0	812	1 PLMN_RAT
25	105	7.8	812	1 PLMN_BOVIN
26	104	7.7	810	1 PLMN_MACMU
27	103	7.6	498	1 YSM5_CAEEL
28	102.5	7.6	942	2 Q182B9
29	101	7.5	810	1 PLMN_HUMAN
30	99.5	7.3	524	2 022815
31	99	7.3	466	2 06TC10

32 99 7.3 510 2 060123 schizosacch
33 99 7.3 693 2 027394 caenorhabdi
34 99 7.3 812 1 PLMN_MOUSE
35 98 7.2 1580 2 07RHE4 plasmidium
36 96.5 7.1 805 1 PLMN_MACEU macrocrob eu
37 96 7.1 627 2 064713 arabidopsis
38 96 7.1 627 2 084150 arabidopsis
39 96 7.1 824 2 066504 oikopleura
40 96 7.1 696 2 061834 caenorhabdi
41 95.5 7.1 615 2 07Q209 giardia lam
42 94.5 7.0 1615 2 07Q2206 bacillus ce
43 94 6.9 429 2 072206 caenorhabdi
44 94 6.9 786 2 062201 caenorhabdi
45 93.5 6.9 480 2 06G2L3 bartonella

ALIGNMENTS

RESULT 1				
ID	001494	PRELIMINARY;	PRT;	1065 AA.
AC	001494;			
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DT	01-DEC-2001 (TREMBREL. 19, Last sequence update)			
DT	01-OCT-2003 (TREMBREL. 25, Last annotation update)			
DB	Hypothetical protein C34G6_6.			
GN	Name=C34G6_6; ORFNames=C34G6_6;			
OS	Caenorhabditis elegans.			
OC	Buclaryota; Metazoa; Nemata; Chromadorea; Rhabditida; Rhabditoidea;			
OX	Rhabditidae; Peleridinae; Caenorhabditis;			
RN	[1]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RT	"Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology. The <i>C. elegans</i> Sequencing Consortium.";			
RL	Science 282:2012-2018(1998).			
RN	[2]			
RP	WormBase Consortium;			
RC	Langston Y., Rohlfing T.;			
RA	"The sequence of the <i>C. elegans</i> cosmid C34G6_6."			
RT	Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.			
RL	[3]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RA	Waterston R.;			
RT	Submitted (DBS-2002) to the EMBL/GenBank/DDBJ databases.			
RL	[4]			
RP	SEQUENCE FROM N.A.			
RC	STRAIN=Bristol N2;			
RG	WormBase Consortium;			
RL	Submitted (SBR-2004) to the EMBL/GenBank/DDBJ databases.			
DR	EMBL: U07407; AAB52479.2; -.			
DR	PIR: C87789; C87789.			
DR	WormBase: WBGene0016422; C34G6_6.			
DR	WormPep: C34G6_6a; CEB9699.			
DR	InterPro: IPR001507; Endoglin/CD105.			
DR	InterPro: IPR030304; PAN.			
DR	InterPro: IPR03609; Pan_app.			
DR	Pfam: Pf00024; PAN_6.			
DR	Pfam: Pf00100; Zoma_peilicida; 1.			
DR	SMART; SM00473; PAN_AP; 6.			
DR	SMART; SM00241; ZP_1.			
DR	PROSITE; PS50948; PAN_6.			
KW	Hypothetical protein.			
SEQUENCE	1065 AA; 117427 MW; DEB597E650648FB4 CRC64;			
Query	Match	67.4%	Score	912.5; DB 2; Length 1065;
Best local Similarity	66.2%	Pred. No.	8.68-76;	

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Db	114	BOKILVGFAREVVSADSVRCLSACTNADTFGECESTVYYPDAECTINTEDRLDRP	60						
QY	61	LFVDEDEHEDVYIUDNCAGCECHHFDKFTSGLINDQFAIA-AQCYAPYVQYAVEG	119						
Db	174	LFVDEDEHEDVYIUDNCAGCECHHFDKFTSGLINDQFAIA-AQCYAPYVQYAVEG	119						
QY	120	RLQSLDELDHSFEGELSECELTQRLSIVANDENCKSMYSNLRSCLSDERSRPLGR	179						
Db	226	RLQSLDELDHSFEGELSECELTQRLSIVANDENCKSMYSNLRSCLSDERSRPLGR	179						
QY	231	PPPETGQNFVCKSMWYNE	250						
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AC	Q8T3B7;								
DT	01-JUN-2002	(TREMBLrel. 21, Created)							
DT	01-JUN-2002	(TREMBLrel. 21, Last sequence update)							
DR	Hypothetical protein C34G6_6.								
GN	Name=C34G6_6; ORFNames=C34G6_6;								
OS	Bukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;								
OC	Caenorhabditida; Peloderrinae; Caenorhabditis; NCBI_TaxID=6239;								
OX	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RX	MEDLINE=99069613; PubMed=9851916;								
RG	WormBase Consortium;								
RT	"Genome sequence of the nematode <i>C. elegans</i> : a platform for investigating biology. The <i>C. elegans</i> Sequencing Consortium.",								
RL	Science 282:2012-2018(1998).								
RN	[1]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Langston Y., Rofiling T.;								
RT	"The sequence of <i>C. elegans</i> cosmid C34G6_6",								
RL	Submitted (APR-1997) to the EMBL/GenBank/DDBJ databases.								
RN	[3]								
RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Waterston R.;								
RL	Submitted (DEC-2002) to the EMBL/GenBank/DDBJ databases.								
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RP	SEQUENCE FROM N.A.								
RC	STRAIN=Bristol N2;								
RA	Matthews P.;								
RL	Submitted (JAN-1996) to the EMBL/GenBank/DDBJ databases.								
DR	EMBL; 268342; CAA92773.1; -.								
DR	PIR; T21967; T21967.								
DR	WormBase; WIGene0009541; F38E11.4.								
DR	WormPep; F38E11.4; CE03296.								
DR	InterPro; IPR001507; Endoglin/CD105.								
DR	InterPro; IPR0030314; PAN.								
DR	InterPro; IPR003609; Pan_app.								
DR	PFam; PF00100; Zona_pellucida, 1.								
DR	SMART; SM0043; PAN_AP; 6.								
DR	InterPro; IPR003104; PAN.								
DR	InterPro; IPR003609; Pan_app.								
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Query	Match	11.8%; Score 160; DB 2; Length 522;	RESULT 7	Match	11.8%; Score 160; DB 2; Length 522;
Best Local Similarity	28.9%; Pred. No. 3	3e-06; Mismatches 71; Indels 18; Gaps 4;	ID	Q22902	PRELIMINARY;
Matches	43; Conservative	17; Mismatches 71; Indels 18; Gaps 4;	ID	Q22902	PRELIMINARY;
QY	112	TOYVAVEGRQLSDELDHSFEGELSERELCTQRLSVTANDRNCKSPMVSNLTRSCVLSD 171	AC	Q22902	PRELIMINARY;
Db	31	TRIFVFTDNASLOSSADPTVYKATSEECLSACTKRNDRKFDRPTVCHSPTYDHSFCTIHK 90	AC	Q22902	PRELIMINARY;
QY	172	ESRPLGRANLAEVPGVTFE -- SRGVV -- SFRIVFQMLVGFASVFMENVPSV 221	DT	01-NOV-1996 (TREMBrel. 01, Created)	DT
Db	91	ESKAPVGSQAQINSVGKRYFECILSHNIPQOCAQTFIRVQSVLGYA - VNMILTDI 149	DT	01-OCT-2003 (TREMBrel. 25, Last sequence update)	DT
QY	222	TMCILDQCTSPPPETGQNPFVCKSVMYYNE 250	GN	Name=C16D9.1; ORFnames=C16D9.1;	GN
Db	150	ESCAAQCV-----QBADCKSAMVYED 171	OS	Caenorhabditis elegans.	OS
QY	222	TMCILDQCTSPPPETGQNPFVCKSVMYYNE 250	OC	Eukaryota; Metazoa; Chromadorea; Rhabditida; Rhabditoidea;	OC
Db	150	ESCAAQCV-----QBADCKSAMVYED 171	OC	Rhabditida; Peleriniae; Cenorhabditis.	OC
RESULT 6			NCBI_TaxID=6239;		
Q7PTF3			[1]		
ID			RP		
AC			SEQUENCE FROM N.A.		
Q7PTF3;					
DT	01-MAR-2004 (TREMBrel. 26, Created)				
DT	01-MAR-2004 (TREMBrel. 26, Last sequence update)				
01-MAR-2004 (TREMBrel. 26, Last annotation update)					
DE	ENSANG000000007588 (Fragment).				
GN	Name=ENSANG000000005132;				
OS	Anopheles gambiae str. PEST.				
OC	Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Nematocera; Culicoidea; Anopheles.				
OX	NCBI_TaxID=180454;				
RN	[1]				
RP	SEQUENCE FROM N.A.				
RA					
RA	Anopheles Genome Sequencing Consortium; EMBL/GenBank/DBJ databases.				
RL	Submitted (APR-2003) to the EMBL/GenBank/DBJ databases.				
CC	-!- CAUTION: The sequence shown here is derived from an preliminary data.				
CC	EMBL; AAB01008807; EAA04001.2; -.				
DR	Int'Pro; IPR001507; Endoglin/CD105.				
DR	InterPro; IPR003014; PAN.				
DR	InterPro; IPR005609; Pan_app.				
DR	Pfam; PF00024; PAN; 5.				
DR	Prosite; P00100; Zona_pellucida; 1.				
FT	NON_TER 1				
SQ	SEQUENCE 1494 AA; 165934 MW; 5CA96D3AR3C24BC1 CRC64;				
Query	Match	11.6%; Score 157; DB 2; Length 1494;			
1	Best Local Similarity	24.6%; Pred. No. 2.3e-05; Mismatches 101; Indels 70; Gaps 14; Matches 67; Conservative			
QY	3	KILVGAREVVSADSVHRCISACLNAAFDTPGFCECESVWYYPVDAECLNTEDRDRPDLF 62			
Db	154	KLPVSDIKEVTAANR-SDCEDKCLN--EPSFVCRSANYDSTLSCMSRFRRTBELL 209			
QY	63	VDEHEDTVYLDNNCAGCECHWHFDNFKTSQGILNDQQFAIAQACIAYPTQVAVEGRL 122			
Db	210	EDDPNSD--YLENCLNNE-----RRCGDLI-----VVVKREKRL 243			
QY	123	SDELD-HSPEGELSECEBLCTORLVSFVANDFCKSFMNSLRSQCVSDB----- 172			
Db	244	GGPFEVEFLFNNNTLEBCSLC-----LRPEKYFCRSIEFDQDQKQCLISEEDSVSQKDL 298			
QY	173	-RSRP-----LGRLAELVPGW-----YFESSRGV--SFRIVFQMLVGFASVFMENVPSV 214			
Db	299	SISSSPTRHYFLVCLDNORGARYPDNSVTSHLFASGRRPTDIAFORVNRSLJGEFHSEI 358			
QY	215	MENVPSPVTMCLDQCTSPPPETGQNPFVCKSVY 246			
Db	359	TGR--SLSCLDECLRQ----TSFOCKSAVY 383			
RESULT 8					
Q8MK23					
ID					
Q8MK23					
AC					
Q8MK23;					
DT	01-OCT-2002 (TREMBrel. 22, Created)				
DT	01-OCT-2002 (TREMBrel. 22, Last sequence update)				

DT 01-MAR-2004 (TREMBrel, 26, last annotation update)

DE CG13207-PC (Cg13207-pd).

GN Name=nompA; ORFNames=CG13207;

OS Drosophila melanogaster (Fruit fly).

OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota; Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha; Ephydriodea; Drosophilidae; Drosophila.

NCBI_TaxID=7227;

RN [1]

SEQUENCE FROM N.A. MEDLINE=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA Adams M.D., Celinker S.E., Holt R.A., Evans C.A., Gocayne J.D.,

RA Amanatides P.G., Scheerer S.E., Li P.W., Hoskins R.A., Galle R.F.,

RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,

RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,

RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,

RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.L.,

RA Abril J.F., Agbayani A., An H.J., Andrews-Pfannkoch C., Baldwin D.,

RA Balow R.M., Basu A., Baxendale J., Byraktaoglu L., Beasley B.M.,

RA Beelew K.Y., Benos P.V., Bernick B.P., Bhandari M., Bolshakov S.,

RA Borkova D., Botchkina M.R., Bouck J., Brodtier P.,

RA Burttis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,

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RA Durbin R.K.J., Evangelista C.C., Ferraz C., Ferreria S., Fleischmann W.,

RA Fosler P., Lei Y., Levinsky A.A., Li J., Li Z., Liang Y., Lin X.,

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RA Hettie D., Houston K.A., Howland T.J., Ibeagwam C.,

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RA Kimmel B.E., Kodira C.D., Kraft C., Kravitz S., Kulp D., Lai Z.,

RA Lasko P., Lei Y., Levinsky A.A., Li J., Li Z., Liang Y., Lin X.,

RA Liu X., Mattel B., McIntosh T.C., McLeod M.P., McPherson D.,

RA Merkulov G., Milshina N.V., Mobarry C., Morris J., Moshrefi A.,

RA Mount S.M., Moy M., Murphy B., Murphy D.M., Nelson D.L.,

RA Nelson D.R., Nelson K.A., Nixon K., Nuskeern D.R., Pacleb J.M.,

RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G.,

RA Reinert H., Remington K., Saunders R.D., Scheeler F., Shen H.,

RA Shue B.C., Siden-Klamm I., Simpson M., Skupski M.P., Smith T.,

RA Siper E., Spradling A.C., Stapleton M., Strong R., Sun E.,

RA Svirkas R., Tector C., Turner R., Venter J.E., Wang A.H., Wang X.,

RA Wang Z.Y., Wasserman D.A., Weinstock G.M., Weissenbach J.,

RA Williams S.M., Woodage T., Worley K.C., Wu D., Yang S., Yao Q.A., Ye J.,

RA Yeh R.F., Zaveri J.S., Zhan M., Zhang Q., Zhao Q., Zheng L.,

RA Zhang X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O.,

RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C.,

RT "Finishing a whole-genome shotgun sequence of *Drosophila melanogaster*,"

RL Science 287:2185-2195 (2000).

RN [2]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426065; PubMed=12537568;

RA Patel S., Adams M., Chang E., Dugan S.P., Fries E., Hodges A.,

RA Celinker S.E., Wheeler D.A., Kronmiller B., Carlson J.W., Halpern A.,

RA George R.A., Hosking R.A., Lavery T., Muzny D.M., Nelson C.R.,

RA Svirkas R., Tabor E., Wan K., Stapleton M., Sutton G.G., Venter C.,

RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.,

RT "Finishing a whole-genome shotgun sequence, Release 3 of the *Drosophila*

RT melanogaster euchromatic genome sequence,"

RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).

RN [3]

RP SEQUENCE FROM N.A.

RX MEDLINE=22426070; PubMed=12537573;

RA Kaminker J.S.S., Bergman C.M., Kronmiller B., Carlson J., Svirkas R., Patel S., Frize E., Wheeler D.A., Lewis S.E., Rubin G.M.,

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RN [4]

SEQUENCE FROM N.A. MEDLINE=22426069; PubMed=12537572;

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SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., Hradecky P., Huang Y., Kaminker J.S., Milburn G.H., Prochnik S.E., Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Bernier B.P., Bettencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A., Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q., Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., Lewis S.B., "Annotation of the *Drosophila melanogaster* euchromatic genome: a systematic review," Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).

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SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase, Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [6]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases.

RN [7]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [8]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [9]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [10]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [11]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [12]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [13]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [14]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [15]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [16]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [17]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [18]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [19]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [20]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [21]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [22]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [23]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [24]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [25]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [26]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [27]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [28]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [29]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [30]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [31]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [32]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [33]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [34]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [35]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [36]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [37]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [38]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [39]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [40]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [41]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [42]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [43]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [44]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [45]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [46]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [47]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [48]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [49]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [50]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [51]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [52]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [53]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [54]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [55]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [56]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [57]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [58]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [59]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [60]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [61]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [62]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [63]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [64]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [65]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [66]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [67]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [68]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [69]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [70]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [71]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [72]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [73]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [74]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [75]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [76]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [77]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [78]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [79]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [80]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [81]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [82]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [83]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [84]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [85]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [86]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [87]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [88]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [89]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [90]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [91]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [92]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [93]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [94]

SEQUENCE FROM N.A. EMBL=2019606; PubMed=10731132; DOI=10.1126/science.287.5451.2185; RX

RA FlyBase; Submitted (SBP-2002) to the EMBL/GenBank/DBJ databases.

RN [95]

SEQUENCE FROM N.A.

RP SSEQUENCE FROM N.A.
 RX MEDLINE=2139724; PubMed=11239432; DOI=10.1016/S0896-6273(01)00215-X;
 RT Chung Y.D., Zhu J., Han Y., Kerman M.J.;
 "nompA encodes a PNS-specific, ZP domain protein required to connect
 mechanosensory dendrites to sensory structures.";
 RL Neuron 29:415-428(2001).
 DR EMBL: AF334032; AAC05434.1; -.
 DR FlyBase; Flygn0016047; nompa.
 DR GO; GO:0007605; P:perception of sound; IMP.
 DR GO; GO:0005929; P:dendrite morphogenesis; TAS.
 DR GO; GO:0007605; P:perception of sound; IMP.
 DR InterPro; IPR001507; Endoglin/CD105.
 DR InterPro; IPR003014; PAN.
 DR Pfam; PF00024; PAN.app.
 DR Pfam; PF00024; PAN; 4.
 DR SMART; SM00473; PAN_AP; 4.
 DR SMART; SM00241; ZP; 1.
 DR PROSITE; PS50948; PAN; 5.
 DR Receptor; Signal.
 FT SIGNAL 1 21 Potential.
 SQ SEQUENCE 1549 AA; 174270 MW; 78C31BAC39D5B93 CRC64;
 Query Match 10.2%; Score 138; DB 2; Length 1549;
 Best Local Similarity 21.2%; Pred. No. 0.0014;
 Matches 58; Conservative 43; Mismatches 100; Indels 72; Gaps 13;
 Qy 3 KILVGFARREVWADSVAHRLCLSACINAFTDFGFECESTMVYPDAECLNTEDRDRPDLF 62
 Db 164 KLPISDIKEITAANR-SDCEDKCLN--EFSTVCRSANFDSTMRSCILSRTTRTHPELM 219
 Qy 63 VDEHEDETYVILDNQAGCSEHWFDFNFKTSGLNDQFAIAACQAYAPVTOVAVEGRL 122
 Db 220 EDDPNSD--VILENTCLNAB-----RRCDG--LAVFVKENKL 253
 Qy 123 SD--ELDHSFEGLEBLSRCEBLCTQRSLVTAMDIFNCKSFMYSNLTRSCVLSRS-RPLGR 179
 Db 254 GCPFEVD-1FNNMTLBCQTCMC-----SRGVPSFTRVQMLLVG-FASSF 307
 Qy 180 ANLAEVPGWVTFE-----SRGVPSFTRVQMLLVG-FASSF 213
 Db 308 ISISSSPTHFVLVLDNQRANDYPDNSVTSHLFSSGRPDTAFQVYNSRIGGEFISSE 367
 Qy 214 VENVPVSPVWCLDQCTSPPPTGPNFVCKSYV 246
 Db 368 ITGR--SLSICIDECIRQ----TSPQCKSAYV 393
 DR
 RESULT 10
 Q9BMD5 PRELIMINARY; PRT; 1557 AA.
 AC Q9BMD5;
 DT 01-JUN-2001 (T:EMBLrel. 17, last sequence update)
 DT 01-JUN-2001 (T:EMBLrel. 17, last annotation update)
 DE No-mechanoreceptor potential A long isoform precursor.
 GN Name-nompA,
 OS Drosophila melanogaster (Fruit fly).
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=2134724; PubMed=11239432; DOI=10.1016/S0896-6273(01)00215-X;
 RX
 RT
 RA Chung Y.D., Zhu J., Han Y., Kerman M.J.;
 "nompA encodes a PNS-specific, ZP domain protein required to connect
 mechanosensory dendrites to sensory structures.";
 RL Neuron 29:415-428(2001).
 DR EMBL: AF334031; AAC05433.1; -.
 DR FlyBase; Flygn0016047; nompa.
 DR GO; GO:0016358; P:dendrite morphogenesis; TAS.
 DR GO; GO:0005929; P:perception of sound; IMP.
 DR InterPro; IPR001507; Endoglin/CD105.
 DR InterPro; IPR003014; PAN.
 DR Pfam; PF00024; PAN.app.
 DR SMART; SM00473; PAN_AP; 4.
 DR SMART; SM00241; ZP; 1.
 DR PROSITE; PS50948; PAN; 5.
 DR Receptor; Signal.
 FT SIGNAL 1 21 Potential.
 SQ SEQUENCE 1557 AA; 175290 MW; 134BBBBAB89245183 CRC64;
 Query Match 10.2%; Score 138; DB 2; Length 1557;
 Best Local Similarity 21.2%; Pred. No. 0.0014;
 Matches 58; Conservative 43; Mismatches 100; Indels 72; Gaps 13;
 Qy 3 KILVGFARREVWADSVAHRLCLSACINAFTDFGFECESTMVYPDAECLNTEDRDRPDLF 62
 Db 164 KLPISDIKEITAANR-SDCEDKCLN--EFSTVCRSANFDSTMRSCILSRTTRTHPELM 219
 Qy 63 VDEHEDETYVILDNQAGCSEHWFDFNFKTSGLNDQFAIAACQAYAPVTOVAVEGRL 122
 Db 220 EDDPNSD--VILENTCLNAB-----RRCDG--LAVFVKENKL 253
 Qy 123 SD--ELDHSFEGLEBLSRCEBLCTQRSLVTAMDIFNCKSFMYSNLTRSCVLSRS-RPLGR 179
 Db 254 GCPFEVD-1FNNMTLBCQTCMC-----SRGVPSFTRVQMLLVG-FASSF 307
 Qy 180 ANLAEVPGWVTFE-----SRGVPSFTRVQMLLVG-FASSF 213
 Db 308 ISISSSPTHFVLVLDNQRANDYPDNSVTSHLFSSGRPDTAFQVYNSRIGGEFISSE 367
 Qy 214 VENVPVSPVWCLDQCTSPPPTGPNFVCKSYV 246
 Db 368 ITGR--SLSICIDECIRQ----TSPQCKSAYV 393
 DR
 RESULT 11
 Q9V5X3 PRELIMINARY; PRT; 1557 AA.
 AC Q9V5X3;
 DT 01-MAY-2000 (T:EMBLrel. 13, Created)
 DT 01-MAY-2000 (T:EMBLrel. 13, Last sequence update)
 DT 01-MAR-2004 (T:EMBLrel. 26, Last annotation update)
 DE CG13207-PA (C013207-pb).
 GN Name-nompA; ORFNames=CG13207;
 OS Drosophila melanogaster (Fruit fly).
 OC Eukaryota; Metazoa; Arthropoda; Hexapoda; Insecta; Pterygota;
 OC Neoptera; Endopterygota; Diptera; Brachycera; Muscomorpha;
 OC Ephydriidae; Drosophilidae; Drosophila.
 RN [1]
 RP SEQUENCE FROM N.A.
 MEDLINE=0196006; PubMed=10731132; DOI=10.1126/science.287.5461.2105;
 RX
 RA Adams M.D., Celniker S.E., Holt R.A., Evans C.A., Gocayne J.D.,
 RA Amanatides P.G., Scherer S.E., Li P.W., Hoskins R.A., Galle R.P.,
 RA George R.A., Lewis S.E., Richards S., Ashburner M., Henderson S.N.,
 RA Sutton G.G., Wortman J.R., Yandell M.D., Zhang Q., Chen L.X.,
 RA Brandon R.C., Rogers Y.H., Blazej R.G., Champe M., Pfeiffer B.D.,
 RA Wan K.H., Doyle C., Baxter E.G., Heit G., Nelson C.R., Gabor G.I.,
 RA Abril J.F., Cawley S., An H.J., Heit G., Nelson C.R., Gabor G.I.,
 RA Balow R.M., Basu A., Baxendale J., Bayraktaroglu L., Beasley E.M.,
 RA Beeson K.Y., Benos P.V., Berman B.P., Bhandari D., Bolshakov S.,
 RA Borkov A., Botchan M.R., Bouck J., Brokstein P., Brottner P.,
 RA Burtis K.C., Busam D.A., Butler H., Cadieu E., Center A., Chandra I.,
 RA Cherry J.M., Cawley S., Dahle C., Davenport L.B., Davies P.,
 RA de Pablo B., Delcher A., Deng Z., Evans A.D., Dew I., Ditzel S.M.,
 RA Dodson K., Doup L.B., Downes M., Dugar-Rocha S., Dunkov B.C., Dunn P.,
 RA Durbin R.K.J., Evangelista C.C., Ferraz C., Ferreira S., Fleischmann W.,
 RA Fosler C., Gabril A.E., Garg W.M., Glaser K.,
 RA Glodek A., Gong F., Gorrell J.H., Gu Z., Guan P., Harris M.,
 RA Harris N.L., Harvey D., Helman T.J., Hernandez J.R., Houck J.,

RA Hostin D., Houston K.A., Howland T.J., Wei M.H., Ibegwam C., DR SMART; SM00241; ZP; 1.
 RA Jalali M., Kalush F., Karpen G.H., Ke Z., Kennison J.A., Kimmell B.E., Kozluk C.D., Kraft C., Kravitz D., Kulp D., Lai Z., DR PROSITE; PS51948; PAN; 5.
 RA Lasko P., Lei Y., Levinsky A.A., Li J., Li Z., Liang Y., Lin X., DR SEQUENCE 1557 AA; MW; E060906D48DB77DF CRC64;
 RA Liu X., Mattel B.Y., McIntosh T.C., McLeod M.P., McPherson D., DR SEQUENCE 10.2%; Score 138; DB 2; Length 1557;
 RA Merkulov G., Milshina N.V., Mobsen J., Moshrefi A., Mount S.M., Moy M., Murphy B., Murphy L., Murzy D.M., Nelson D.L., DR Best Local Similarity 21.2%; Pred. No. 0.0014; Mismatches 58; Conservative 43; MisMatches 100; Indels 72; Gaps 13;
 RA Nelson D.R., Nelson K.A., Nixon S., Nusbekern D.R., Pacleb J.M., DR SEQUENCE 1557 AA; MW; E060906D48DB77DF CRC64;
 RA Palazzolo M., Pittman G.S., Pan S., Pollard J., Puri V., Reese M.G., DR Query Match 3; KILYGFAR3VVSADSUVHRLSACINAFDFTGFBCESVMYYPVDAECLNTEDRDRPDLF 62;
 RA Reinert K., Remington K., Saunders R.D., Scheeler F., Shen H., DR Matches 3; KILYGFAR3VVSADSUVHRLSACINAFDFTGFBCESVMYYPVDAECLNTEDRDRPDLF 62;
 RA Shue B.C., Sisden-Klamas I., Simpson M., Skupski M.P., Smith T., DR Spier E., Spradling A.C., Stapleton M., Strong R., Sun E.,
 RA Svartkas R., Tector C., Turner R., Venter E., Wang A.H., Wang X., DR 164 KLIPSDIKLTAAKR-SDCEDKCLN--EFSFVCRSANFDSRSCSLSRTRRTHPELM 219;
 RA Wang Z.Y., Wasbarman D.A., Weinstock G.M., Weissenbach J., DR QY 63 VDEHEDTVYILDNNCAGGCHWHDNPKNSGILNDQQPFIQIAQCYAPVYQVAVGROL 122;
 RA Williams S.M., Woodage T., Worley T., Wu D., Yeung S., Yau Q.A., Ye J., DR QY 123 SD--ELDHSFEGGLESECEFLCTORLVSIVANDENICKSFYNSNLSNTRSCVSDERS-RPLGR 179;
 RA Yeh R.F., Zaveri J.S., Zhan M., Zhang G., Zhao Q., Zheng L., DR QY 220 EDDPNSD-YLENLCLNAE-----RRCDG--LAUVEKEENKLRL 253;
 RA Zheng X.H., Zhong F.N., Zhong W., Zhou X., Zhu S., Zhu X., Smith H.O., DR RT 254 GGPFEVD-1FNNWMLBECQMC---LRAEKYFCRSVFEFFDQSKQCISSEESISQDD 307;
 RA Gibbs R.A., Myers E.W., Rubin G.M., Venter J.C., DR RN [2];
 RA Weinstock G., Scherer S.E., Myers E.W., Gibbs R.A., Rubin G.M.; DR RT "true genome sequence of *Drosophila melanogaster*.";
 RA Celniker S.E., Wheeler D.A., Kromiller B., Carlson J.W., Halpern A., DR RN Science 287:2185-2195 (2000).
 RA Patel S., Adams M., Champe M., Dugan S.P., Frise E., Hodgson A., DR RP SEQUENCE FROM N.A.
 RA Frise E., Wheeler D.A., Laverty T., Muzny D.M., Nelson C.R., DR RN MEDLINE-22426065; PubMed=12537568;
 RA Pacieb J.M., Park B.D., Preiffer B.D., Richards S., Sodergren E.J., DR RT "the transposable elements of the *Drosophila melanogaster* euchromatin: a genomics perspective";
 RA Svirskas R., Tabor P.E., Wan K., Stapleton M., Sutton G.G., Venter C., DR RL "Finishing a whole-genome shotgun. Release 3 of the *Drosophila melanogaster* euchromatic genome sequence.,";
 RA Celniker S.E., Wheeler D.A., Kromiller B., Carlson J.W., Halpern A., DR RL Genome Biol. 3:RESEARCH0079-RESEARCH0079 (2002).
 RN [3];
 RP SEQUENCE FROM N.A.
 RX MEDLINE-22426070; PubMed=12537572;
 RA Kaminer J.S., Bergman C.M., Kromiller B., Carlson J., Svirskas R., DR AC Q21782 PRELIMINARY; PRT; 351 AA.
 RA Patel S., Frise E., Wheeler D.A., Lewis S.E., Rubin G.M., DR DT 01-NOV-1996 (TREMBrel. 01, Created)
 RA Ashburner M., Celniker S.E., DR DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 RT "the transposable elements of the *Drosophila melanogaster* euchromatin: a genomics perspective";
 RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
 RN [4];
 RP SEQUENCE FROM N.A.
 RX MEDLINE-22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S., DR AC Q21782 PRELIMINARY; PRT; 351 AA.
 RA Hradecky P., Huang Y., Kaminer J.S., Millburn G.H., Prochnik S.E., DR DT 01-NOV-1996 (TREMBrel. 01, Last sequence update)
 RA Smith C.D., Tupy J.L., Whitfield E.J., Bayraktaroglu L., Berman B.P., DR DT 01-MAR-2004 (TREMBrel. 26, Last annotation update)
 RA Babbencourt B.R., Celniker S.E., de Grey A.D., Drysdale R.A., DR DE Hypothetical protein R07A4.4;
 RA Harris N.L., Richer J., Russo S., Schroeder A.J., Shu S.Q., DR GN ORFName=R07A4.4;
 RA Stapleton M.M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M., DR OS Caenorhabditis elegans.
 RA Lewis S.E.; DR OC Eukaryota; Metazoa; Nematoda; Chromadorea; Rhabditida; Rhabditoidea;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a DR RC Rhabditidae; Peloderrinae; Caenorhabditis.
 RL Genomic Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
 RN [5];
 RP SEQUENCE FROM N.A.
 RG Submitted (SSBP-2002) to the EMBL/GenBank/DBJ databases. DR SEQUENCE FROM N.A.
 RL STRAIN=Bristol N2; DR RC
 RN MEDLINE-99069613; PubMed=9851916; DR RT investigating biology";
 RA none; DR RL Science 282:2012-2018 (1998).
 RT "Genome sequence of the nematode *C.elegans*: A platform for DR RN [2];
 RC SEQUENCE FROM N.A.
 RC STRAIN=Bristol N2; DR RT investigating biology";
 RA Cottage A.; DR RL Submitted (Nov-1995) to the EMBL/GenBank/DBJ databases.
 RG Submitted (MAR-2004) to the EMBL/GenBank/DBJ databases. DR DR EMBL; Z07756; CA91764.1; -. DR
 RL Submitted (SSBP-2002) to the EMBL/GenBank/DBJ databases. DR DR InterPro; IPR001507; Endoglin/CD105.
 DR InterPro; IPR003047; nomPA. DR DR InterPro; IPR001507; Endoglin/CD105.
 DR InterPro; IPR003047; nomPA. DR DR InterPro; IPR001507; Endoglin/CD105.
 DR GO:0016539; P: dendrite morphogenesis; T: AS. DR DR InterPro; IPR001507; Endoglin/CD105.
 DR GO:0009532; P: detection of sound; IMP. DR DR InterPro; IPR001507; Endoglin/CD105.
 DR GO: GO:0007605; P: perception of sound; IMP. DR DR InterPro; IPR003669; Pan app.
 DR InterPro; IPR001507; Endoglin/CD105. DR DR InterPro; IPR003669; Pan app.
 DR InterPro; IPR003669; Pan app. DR DR InterPro; IPR003669; Pan app.
 DR InterPro; IPR003669; Pan app. DR DR InterPro; IPR003669; Pan app.
 DR InterPro; IPR003669; Pan app. DR DR InterPro; IPR003669; Pan app.
 DR InterPro; IPR003669; Pan app. DR DR InterPro; IPR003669; Pan app.
 DR InterPro; IPR003669; Pan app. DR DR InterPro; IPR003669; Pan app.
 DR SMART; SM00473; PAN_AP; 4. DR DR InterPro; IPR003669; Pan app.
 DR SMART; SM00473; PAN_AP; 4. DR DR InterPro; IPR003669; Pan app.
 DR SMART; SM00473; PAN_AP; 4. DR DR InterPro; IPR003669; Pan app.

RL Genome Biol. 3:RESEARCH0084-RESEARCH0084 (2002).
 RN [14]
 RP SEQUENCE FROM N.A.
 RX MEDLINE=22426069; PubMed=12537572;
 RA Misra S., Crosby M.A., Mungall C.J., Matthews B.B., Campbell K.S.,
 RA Hradecky P., Huang Y., Mungall J.S., Mattioli B., Millburn G.H., Prochnik S.E.,
 RA Smith C.D., Tupy J.L., Whitfield E.J., Byraktaoglu L., Berman B.P.,
 RA Bettencourt B.R., Celinker S.E., de Grey A.D., Drysdale R.A.,
 RA Harris N.L., Richter J., Russo S., Schroeder A.J., Shu S.Q.,
 RA Stapleton M., Yamada C., Ashburner M., Gelbart W.M., Rubin G.M.,
 RA Lewis S.E.;
 RT "Annotation of the *Drosophila melanogaster* euchromatic genome: a
 systematic review.";
 RL Genome Biol. 3:RESEARCH0083-RESEARCH0083 (2002).
 RN [15]
 RP SEQUENCE FROM N.A.
 RG FlyBase; Submitted (SEP-2002) to the EMBL/GenBank/DDBJ databases.
 RN [16]
 RP SEQUENCE FROM N.A.
 RG FlyBase;
 RL Submitted (MAR-2004) to the EMBL/GenBank/DDBJ databases.
 RN [17]
 RP SEQUENCE FROM N.A.
 RC STRAIN=Berkeley;
 RA Stapleton M., Brokstein P., Hong L., Agbayani A., Carlson J.,
 RA Champe M., Chavez C., Dorsett V., Dresnek D., Fairman D., Fries E.,
 RA George R., Gonzalez M., Guarin H., Krommiller B., Li P., Liao G.,
 RA Miranda A., Mungall C.J., Munoz J., Paclob J., Paragas V., Park S.,
 RA Patel S., Phouanenavong S., Wan K., Yu C., Lewis S.E., Rubin G.M.,
 RA Celinker S.;
 RL Submitted (APR-2002) to the EMBL/GenBank/DDBJ databases.
 DR EMBL; AE003771; AAF66948; 1; -.
 DR EMBL; AY034725; AAM11078; 1; -.
 DR FlyBase; FBgn0039704; CG7802.
 DR InterPro; IPR001507; Endoglucanase_C105.
 DR InterPro; IPR003014; PAN.
 DR InterPro; IPR003609; Pan_app.
 DR Pfam; PF00024; PAN; 3.
 DR SMART; SM00473; PAN_AP; 3.
 DR SMART; SM00241; ZP; 1.
 DR FROSTIE; PS50948; PAN; 3.
 DR SEQUENCE; 744 AA; 83086 MW; FD2403A63FF75FFBE CRC64;
 > Query Match Similarity 8.9%; Score 121; DB 2; Length 744;
 Best Local Similarity 23.4%; Pred. No. 0.022; Mismatches 102; Indels 78; Gaps 14;
 Matches 64; Conservative 29; Mismatches 102; Indels 78; Gaps 14;
 QY 5 LVGPAERPVVA-----DS-----VHRCISACLNAPDFGPFECESVMMYYPDAEC 48
 DB 117 LVGF--BIVTGYVFSAPEBKLMDSQPGTMLMUTCDPDKR---NKTQSVNYY--ETGLC 167
 QY 49 IINTEIDLDRD-LFVDBHEITIVYKLDNNCAG--CECHWHFDNFKTSGLNDQOFAIA 104
 DB 168 VLFSAHADQLGGALTQSKQPVFTIVAQKSCLAVKQCSRRAWYDR----- 211
 105 QCYAPVYTQYVAVEGRQLSDFLIDHSPEGLSECEBLCTORLSVTANDFNCKSFMSNLT 164
 DB 212 -----VQNYKLUKEKRTVSVASRRCFBLC----LGENDFTCRSANIDRTS 254
 QY 165 RSCVNSDERSRPLGRANLAEV-PGWTYFESRGVP-----SFRTPQMLVGFASFYME 217
 DB 255 GACELSELDRLTLAGSQAQFOVNDGSDYLENHICVDESPNKLCKRLPGRILKTVDS-VYQE 313
 QY 218 VPSVTVMLQDQTSPPPETGQFWCKSVMMYME 250
 DB 314 VVSIDBCRELCLNSP-----YRCHS--YDND 338

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